

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: September 21, 2004, 20:24:10 ; Search time 303 Seconds

(without alignments)

5742.244 Million cell updates/sec

Title:

US-09-774-490-1

Perfect score: 895

Sequence: 1 aatcttttttttcgatg.....aggcttttttttcctaaacc 2709

Scoring table:

OLIGO	Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 1342398 seqs, 32113274 residues

Word size: 1

Total number of hits satisfying chosen parameters: 2578168

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p.model -DEV=xlp

-Q=/cgn2_1/USPTO.spool_p/US09774490/runat_21092004_144323_2648/app_query.fasta_1.2887

-DB=publishedApplications AA -QFM=fastan -SUFFIX=oligo.rapb -MINMATCH=0.1

-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=cligo

-TRANS=human40.cdi -LIST=45 -DOCLIGN=200 -THR SCORE=quality -THR MIN=1

-ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0

-MAXLEN=2000000000 -USER=US09774490 @CGN 1.1.453 @runat_21092004_144323_2648

-NCPU=6 -ICPU=3 -NO.WMAP -LARGEQUEY -NEG SCORE=0 -WAIT -DSBBLCK=100

-LONGLOG -DSV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60

-XGAPOP=6 -XGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : Published Applications AA:

1:	/cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2:	/cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3:	/cgn2_6/ptodata/2/pubpaa/US66_NEW_PUB.pep.*
4:	/cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5:	/cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6:	/cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7:	/cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8:	/cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9:	/cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10:	/cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11:	/cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12:	/cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13:	/cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14:	/cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15:	/cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16:	/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
17:	/cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
18:	/cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
------------	-------	-------	--------	----	-------------

771	86.1	771	14	US-10-097-340-284	Sequence 284, App
771	86.1	771	14	US-10-262-538-10	Sequence 10, Appl
771	86.1	771	14	US-10-067-632-54	Sequence 54, Appl
771	86.1	771	14	US-10-247-671-164	Sequence 164, Appl
655	73.2	655	14	US-10-320-769-3	Sequence 3, Appl
151	16.9	151	9	US-09-864-761-47112	Sequence 47112, A
100	11.2	100	12	US-09-773-876-5	Sequence 5, Appl
54	6.0	54	14	US-10-029-386-30748	Sequence 30748, A
53	5.9	57	9	US-09-864-761-44075	Sequence 44075, A
53	5.9	60	14	US-10-029-386-29372	Sequence 29372, A
41	4.6	41	9	US-09-864-761-44552	Sequence 44552, A
33	3.7	33	9	US-09-864-761-39708	Sequence 39708, A
17	1.9	779	9	US-09-731-179-2	Sequence 2, Appl
17	1.9	782	9	US-09-813-290-4	Sequence 4, Appl
15	1.7	875	9	US-09-813-290-2	Sequence 2, Appl
15	1.7	514	12	US-10-357-820-28	Sequence 28, Appl
15	1.7	636	16	US-10-408-765A-2003	Sequence 2003, Ap
15	1.7	749	14	US-10-263-538-12	Sequence 12, Appl
15	1.7	749	14	US-10-285-351B-1	Sequence 1, Appl
15	1.7	751	13	US-10-114-893-214	Sequence 214, App
15	1.7	751	14	US-10-060-036-172	Sequence 172, App
15	1.7	751	14	US-10-205-823-359	Sequence 359, App
15	1.7	751	14	US-10-262-538-14	Sequence 14, Appl
14	1.6	777	10	US-09-946-374-310	Sequence 310, Appl
14	1.6	777	12	US-10-206-915-348	Sequence 348, App
14	1.6	777	12	US-10-199-670-348	Sequence 348, App
14	1.6	777	12	US-10-201-858-348	Sequence 348, App
14	1.6	777	12	US-10-205-890-348	Sequence 348, App
14	1.6	777	12	US-10-208-024-348	Sequence 348, App
14	1.6	777	12	US-10-201-853-348	Sequence 348, App
14	1.6	777	12	US-10-174-581-348	Sequence 348, App
14	1.6	777	12	US-10-176-483-348	Sequence 348, App
14	1.6	777	12	US-10-176-749-348	Sequence 348, App
14	1.6	777	12	US-10-176-914-348	Sequence 348, App
14	1.6	777	12	US-10-176-915-348	Sequence 348, App
14	1.6	777	12	US-10-006-485A-310	Sequence 310, App
14	1.6	777	12	US-10-013-907A-310	Sequence 310, App
14	1.6	777	12	US-10-015-499A-310	Sequence 310, App
14	1.6	777	12	US-10-176-484-348	Sequence 348, App
14	1.6	777	12	US-10-180-550-348	Sequence 348, App
14	1.6	777	12	US-10-183-014-348	Sequence 348, App
14	1.6	777	12	US-10-187-738-348	Sequence 348, App
14	1.6	777	12	US-10-187-740-348	Sequence 348, App
14	1.6	777	12	US-10-187-883-348	Sequence 348, App
14	1.6	777	12	US-10-194-363-348	Sequence 348, App

ALIGNMENTS

RESULT 1

US-10-097-340-284
; Sequence 284, Application US/10097340
; Publication No. US20030087250A1
; GENERAL INFORMATION:
; APPLICANT: JOHN MCNAHAN
; APPLICANT: Manjula GANNAVARAPU
; APPLICANT: Sebastian HOERSCH
; APPLICANT: Shubhangi KAMATKAR
; APPLICANT: Steve G. KOVATS
; APPLICANT: Rachel E. MEYERS
; APPLICANT: Michael MORRISSEY
; APPLICANT: Peter OLANDT
; APPLICANT: Ami SEN
; APPLICANT: Peter VEIBY
; APPLICANT: Gordon B. MILLS
; APPLICANT: Robert C. EAST, Jr.
; APPLICANT: Karen LU
; APPLICANT: Rosemarie SCHMANDT
; APPLICANT: Xumei ZHAO
; APPLICANT: Karen GLATT
; TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
; TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
; FILE REFERENCE: MRI-030

; CURRENT APPLICATION NUMBER: US/10/097,340
 ; CURRENT FILING DATE: 2002-03-14
 ; PRIOR APPLICATION NUMBER: 60/276,025
 ; PRIOR FILING DATE: 2001-03-14
 ; PRIOR APPLICATION NUMBER: 60/325,149
 ; PRIOR FILING DATE: 2001-09-26
 ; PRIOR APPLICATION NUMBER: 60/276,026
 ; PRIOR FILING DATE: 2001-03-14
 ; PRIOR APPLICATION NUMBER: 60/324,967
 ; PRIOR FILING DATE: 2001/09/26
 ; PRIOR APPLICATION NUMBER: 60/311,732
 ; PRIOR FILING DATE: 2001-08-10
 ; PRIOR APPLICATION NUMBER: 60/325,102
 ; PRIOR FILING DATE: 2001-09-26
 ; PRIOR APPLICATION NUMBER: 60/323,580
 ; PRIOR FILING DATE: 2001-09-19
 ; NUMBER OF SEQ ID NOS: 363
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 284
 ; LENGTH: 771
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-097-340-284

Alignment Scores:

Pred. No.: 0 Length: 771
 Score: 771.00 Matches: 771
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 86.15% Indels: 0
 DB: 14 Gaps: 0

US-09-774-490-1 (1-2709) x US-10-097-340-284 (1-771)

QY 200 ATGGGCTGTTAACTAGGATTCCTCTTTCTGGGAGTATTACTTTACAGCAGAGCA 259
 Db 1 MetGlyTrpLeuThrArgIleValCysLeuPheTrpGlyValLeuLeuThrAlaArgAla 20
 QY 260 AACTATCAGAAATGGGAGAACAAATGTCCAGGCTGAATATATCTCAAGAAATGTTG 319
 Db 21 AsnTyrGlnAsnGlyLysAsnValProArgLeuLysLeuSerTyrLysGluMetLeu 40
 QY 320 GAATCCAAATGTGATCACTTTCAATGCTTGGCCACAGCTCCAGTTATCATACCTTC 379
 Db 41 GluSerAsnValIleThrPheAsnGlyLeuAlaAsnSerSerTyrHisThrPhe 60
 QY 380 CTTTGGATGAGAACCGAGTAGGCTGTATGTGGAGCAAGAGTATCATATTTTCATTC 439
 Db 61 LeuLeuAspGluArgSerArgLeuTyrValGlyAlaLysAspHisIlePheSerPhe 80
 QY 440 GACCTGTTAATCAAGGATTTTCAAGAGATTGTGGCCAGTATCTTACACCAGAGA 499
 Db 81 AspLeuValAsnIleLysAspPheGlnLysIleValTrpProValSerTyrThrArgArg 100
 QY 500 GATGAATGCAATGGGCTGGAAGAACATCTGGAAGAAATGTCTAATTCATCAAGGTA 559
 Db 101 AspGluCysLysTrpAlaGlyLysAspIleLeuLysGluCysAlaAsnPheIleLysVal 120
 QY 560 CTTAAGGCATATAATCAGACTCACCTTGACCTGTGGAGCGGGCTTTTCATCCAAAT 619
 Db 121 LeuLysAlaTyrAsnGlnThrHisLeuTyrAlaCysGlyThrGlyAlaPheHisProIle 140
 QY 620 TGCACCTAATTAATTTGGACATCATCTGAGACAAATATTTTAAGCTGGAGAACTCA 679
 Db 141 CysThrTyrIleGluIleGlyHisHisProGluAspAsnIlePheLysLeuGluAsnSer 160
 QY 680 CATTTTGAAGCGCGGTGGGAGAGTCCATATGACCTCAAGCTGCTGACAGATCCCTT 739
 Db 161 HisPheGluAsnGlyArgGlyLysSerProTyrAspProLysLeuLeuThrAlaSerLeu 180
 QY 740 TTAATAGATGGAGAAATTAATCTCTGGAACTGACGACTATTTATGGGCGAGACTTTGCT 799
 Db 181 LeuIleAspGlyGluLeuTyrSerGlyThrAlaAlaAspPheMetGlyArgAspPheAla 200

QY 800 ATCTTCCGAAGTCTTTGGGCACCAACCAATCAGGACAGAGCAGCATGATTCAGGTGG 859
 Db 201 IlePheArgThrLeuGlyHisHisProIleArgThrGluGlnHisAspSerArgTrp 220
 QY 860 CTCATATGATCCAAAGTTCATTAGTGGCCACCTCATCTCAGAGAGTGACATCTGAGAT 919
 Db 221 LeuAsnAspProLysPheIleSerAlaHisLeuIleSerGluSerAspAsnProGluAsp 240
 QY 920 GACAAAGTATATCTTTCTTCGTCGAAAATGCAATAGATCGAGAACACTCTGCAAGCT 979
 Db 241 AspLysValTyrPhePhePheArgGluAsnAlaIleAspGlyGluHisSerGlyLysAla 260
 QY 980 ACTCAGCTAGATAGTTCAGATATGCAAGATGACTTTGGAGGCACAGAACTCTGGT 1039
 Db 261 ThrHisAlaArgIleGlyGlnIleCysLysAsnAspPheGlyGlyHisArgSerLeuVal 280
 QY 1040 AATAAATGACACACATTCCTCAAGCTCGTCTGATTTGCTCAGTGGCAGGTCCAAATGGC 1099
 Db 281 AsnLysTrpThrThrPheLeuLysAlaArgLeuIleCysSerValProGlyProAsnGly 300
 QY 1100 ATTGACACTCATTTTGATGAACCTCAGGATGTATTCCTATGAACCTTAAAGATCTCTAA 1159
 Db 301 IleAspThrHisPheAspGluLeuGlnAspValPheLeuMetAsnPheLysAspProLys 320
 QY 1160 AATCCAGTGTATATGGAGTGTATTACGACTTCAGTAAACATTTTCAAGGATCAGCGGTG 1219
 Db 321 AsnProValValTyrGlyValPheThrThrSerSerAsnIlePheLysGlySerAlaVal 340
 QY 1220 TGTATGATAGCATGAGTATGAGAGGGTGTCTCTGTCATATGCCACAGGAT 1279
 Db 341 CysMetTyrSerMetSerAspValArgArgValPheLeuGlyProTyrAlaHisArgAsp 360
 QY 1280 CGACCCAACTAATCAATGGTGCCTTATCAAGGAGAGTCCCTCATCAAGGCGAGAACT 1339
 Db 361 GlyProAsnTyrGlnTrpValProTyrGlnGlyArgValProTyrProArgProGlyThr 380
 QY 1340 TGTCCAGCAAAATTTGGTGTGTTTGACTCTACAAAGGACCTTCTGATGATGTTATA 1399
 Db 381 CysProSerTyrThrPheGlyGlyPheAspSerThrLysAspLeuProAspAspValIle 400
 QY 1400 ACCTTTGCAGAAAGTCAATCCAGCATGTACAAATCCAGTGTTCCTATGAACTATCCCA 1459
 Db 401 ThrPheAlaArgSerHisProAlaMetTyrAsnProValPheProMetAsnAsnArgPro 420
 QY 1460 ATAGTATCAAAACCGATGTAAATTTATCAATTTTACAAATTTGCTGTAGACCGAGTGGAT 1519
 Db 421 IleValIleLysThrAspValAsnTyrGlnPheThrGlnIleValValAspArgValAsp 440
 QY 1520 GCAGAAAGATGACAGTATGATGTTTATCGGACACAGATGTTGGACCGCTTCTTAA 1579
 Db 441 AlaGluAspGlyGlnTyrAspValMetPheIleGlyThrAspValGlyThrValLeuLys 460
 QY 1580 GTAGTTTCAATTCCTAAGGAGACTTGTGTATGATTTAGAGAGGTTCCTCTGGAGAAATG 1639
 Db 461 ValValSerIleProLysGluThrTrpTyrAspLeuGluValValLeuLeuGluMet 480
 QY 1640 ACAGTTTTTTCGGGAACCGACTGCTTATTTACAGCAATGGAGCTTTCCACTAAGCAGCAACA 1699
 Db 481 ThrValPheArgGluProThrAlaIleSerAlaMetGluLeuSerThrLysGlnGln 500
 QY 1700 CTATATATTTGTTCAACGGCTGGGGTGGCCAGCTCTTACACCGGTGTATATTTAC 1759
 Db 501 LeuTyrIleGlySerThrAlaGlyValAlaGlnLeuProLeuHisArgCysAspIleTyr 520
 QY 1760 GGGAAAGCGTGTGTGAGTGTGCTCGCCCGAGAGCCCTTACTGTCTTGGATGTTCT 1819
 Db 521 GlyLysAlaCysAlaGluCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlySer 540
 QY 1820 GCATGTTCTGCTATTTTCCACTGCAAGAGACGACAGCAGCAGCAAGATATAGAAAT 1879
 Db 541 AlaCysSerArgTyrPheProThrAlaLysArgArgThrArgGlnAspIleArgAsn 560

```
QY 1880 GGAGACCCAGTCACTCACTGTTAGACTTACACCATGATATACCATGCGCCAGCCCT 1939
Db 561 GlyAspProLeuThrHisCysSerAspLeuHisHisAspAsnHisHisGlyHisSerPro 580
QY 1940 GAAAGAGAAATCATCTATGTTGTAGAGAAATAGTACACATTTTGGGAATGCACTCCGAAG 1999
Db 581 GluGluArgIleIleTyrGlyValGluAsnSerSerThrPheLeuGluCysSerProLys 600
QY 2000 TCGCAGAGAGGCTGGTCTATTGGCAATTCAGAGGGGAAATGAAGAGCGAAGAAGAG 2059
Db 601 SerGlnArgAlaLeuValTyrTrpGlnPheGlnArgArgAsnGluGluArgLysGluGlu 620
QY 2060 ATCAGAGTGGATGATCATATCATCAGGACACATCAAGGCCCTTCCTGCTACGTAGTCTCAA 2119
Db 621 IleArgValAspAspHisIleIleArgThrAspGlnGlyLeuLeuLeuArgSerLeuGln 640
QY 2120 CAGAAGGATTGAGCAATTAATCTGTCATCGGATGGTGAACATGGGTTTCATACAACTCTT 2179
Db 641 GlnLysAspSerGlyAsnTyrLeuCysHisAlaValGluHisGlyPheIleGlnThrLeu 660
QY 2180 CTTAAGGTAACCTCGGAGTCAATTCAGACAGACATTTGGGAACATCTTCATAAAGAT 2239
Db 661 LeuLysValThrLeuGluValIleAspThrGluHisLeuGluGluLeuLeuHisLysAsp 680
QY 2240 GATGATGAGATGGCTCTTAAGCAACAAAGAAATGTCCAATAGCATGACACCTAGCCAGAAG 2299
Db 681 AspAspGlyAspGlySerLysThrLysGluMetSerAsnSerMetThrProSerGlnLys 700
QY 2300 GTCTGGTACAGAGATTCATGACGCTCATCAACACCCCAATCTCAACAGATGATGAG 2359
Db 701 ValTrpTyrArgAspPheMetGlnLeuIleAsnHisProAsnLeuAsnThrMetAspGlu 720
QY 2360 TTCTGTGAACCAAGTTTGGAAAGGAGCCGAAACAAAGTCGGCAAGCCAGGACATACC 2419
Db 721 PheCysGluGlnValTrpLysArgAspArgLysGlnArgGlnArgProGlyHisThr 740
QY 2420 CCAGGGAACAGTACAAATGGAAGCATTACAGAAATAGAAAGGTAGAAACAGGAGG 2479
Db 741 ProGlyAsnSerAsnLysTrpLysHisLeuGlnGluAsnLysLysGlyArgAsnArg 760
QY 2480 ACCCAGCAATTTGAGAGGACCCAGGAGTGTC 2512
Db 761 ThrHisGluPheGluArgAlaProArgSerVal 771

RESULT 2
US-10-262-538-10
; Sequence 10, Application US/10262538
; Publication No. US2003011324A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo et al
; TITLE OF INVENTION: NEUROPILIN/VEGF-C/VEGFR-3 MATERIALS AND METHODS
; FILE REFERENCE: 28967/37564
; CURRENT APPLICATION NUMBER: US/10/262,538
; CURRENT FILING DATE: 2002-09-30
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 771
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-262-538-10

Alignment Scores:
Pred. No.: 0 Length: 771
Score: 771.00 Matches: 771
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 86.15% Indels: 0
DB: 14 Gaps: 0

US-09-774-490-1 (1-2709) x US-10-262-538-10 (1-771)
QY 200 ATGGGCTGGTAACTAGGATGTCTGCTTTTCTGGGAGTATTACTTACAGCAAGACGA 259
```

```
Db 1 MetGlyTrpLeuThrArgIleValCysLeuPheTrpGlyValLeuLeuThrAlaArgAla 20
QY 260 AACTATCAGAAATGGGAAGAACAAATGTGCCAAGCTGAAATTAATTCCTACAAAGAAATGTTG 319
Db 21 AsnTyrGlnAsnGlyLysAsnAsnValProArgLeuLysLeuSerTyrLysGluMetLeu 40
QY 320 GAATCCAAATGTGATCACTTTCAATGGCTTGGCCACAGCTCCAGTTATCATCCTTC 379
Db 41 GluSerAsnAsnValIleThrPheAsnGlyLeuAlaAsnSerSerTyrHisThrPhe 60
QY 380 CTTTTCGATCAGAAACGAGTAGGCTGTATGTGGAGCAAAAGATCACATATTTTCATTC 439
Db 61 LeuLeuAspGluGluArgSerArgLeuTyrValGlyAlaLysAspHisIlePheSerPhe 80
QY 440 GACCTGGTTAATATCAAGATTTTCAAAGATTTGTGCCAGTATCTTACACCCAGAGA 499
Db 81 AspLeuValAsnIleLysAspPheGlnLysIleValTrpProValSerTyrThrArgArg 100
QY 500 GATGAATGCAAGTGGCTCGAAAAGACATCTCTGAAAGAAATGTCTTAATTTTCATCAAGTGA 559
Db 101 AspGluCysLysTrpAlaGlyLysAspIleLeuLysGluCysAlaAsnPheIleLysVal 120
QY 560 CTTAAGGCATATAATCAGACTCACTGTGTAGGCTGTGGAAACGGGGCTTTTCATCCAAT 619
Db 121 LeuLysAlaTyrAsnGlnThrHisLeuTyrAlaCysGlyThrGlyAlaPheHisProIle 140
QY 620 TGCACCTACATTAATTCGATCATCTCTGAGGACAAATATTTTAAAGTCGAGAACTCA 679
Db 141 CysThrTyrIleGluIleGlyHisHisProGluAspAsnIlePheLysLeuGluAsnSer 160
QY 680 CATTTTGAACACGGCTGGGAAGAGTCCATATGACCCCTAAGCTGCTGACAGATCCCTT 739
Db 161 HisPheGluAsnGlyArgGlyLysSerProTyrAspProLysLeuLeuThrAlaSerLeu 180
QY 740 TTAATAGATGGGAATATATCTCGAAGTGCAGCTGATTTTATGGGGGAGACACTTTGCT 799
Db 181 LeuIleAspGlyGluLeuTyrSerGlyThrAlaAlaAspPheMetGlyArgAspPheAla 200
QY 800 ATCTTCCGAACTCTTGGGACACCCACCAATCAGACAGACAGACAGATATTCAGAGTGG 859
Db 201 IlePheArgThrLeuGlyHisHisHisProIleArgThrGluGlnHisAspSerArgTrp 220
QY 860 CTCATATGATCCAAAGTTCATTTAGTGCCTCCACCTCATCTCAGAGAGTGACAAATCCTGAGAT 919
Db 221 LeuAsnAspProLysPheIleSerAlaHisLeuIleSerGluSerAspAsnProGluAsp 240
QY 920 GACAAAGTATACTTTTCTTCCTGAAATGCAATAGATGGAGAACACACTCTGAAAAGCT 979
Db 241 AspLysValTyrPhePhePheArgGluAsnAlaIleAspGlyGluHisSerGlyLysAla 260
QY 980 ATCCACGCTAGAAATAGTTCAGATATGCAAGAATGACTTTGGAGGGGCACAGAGTCTGGTG 1039
Db 261 ThrHisAlaArgIleGlyGlnIleCysLysAsnAspPheGlyGlyHisArgSerLeuVal 280
QY 1040 AATAATGGACACATTCCTCAAGCTCGTCTGATTTGCTCAGTGCACAGTCCCAATGCG 1099
Db 281 AsnLysTrpThrThrPheLeuLysAlaArgLeuIleCysSerValProGlyProAsnGly 300
QY 1100 ATTGACACTCATTTTCATCACTGAGGATGTATTCCTAATGAACCTTTAAAGATCCATAA 1159
Db 301 IleAspThrHisPheAspGluLeuGlnAspValPheLeuMetAsnPheLysAspProLys 320
QY 1160 AATCCAGTTGTATATGAGTGTTTAGACTTCAGTAACTATTCAGGGGATCAGCCGTG 1219
Db 321 AsnProValValTyrGlyValPheThrThrSerSerAsnIlePheLysGlySerAlaVal 340
QY 1220 TGTATGTATAGCATGATGTGAGAAGGGTTCCTTGGTCCATATATCCACACAGGAT 1279
Db 341 CysMetTyrSerMetSerAspValArgValPheLeuGlyProTyrAlaHisArgAsp 360
QY 1280 GGCACCAACTATCAATGGGTGCTTATCAAGGAAGAGTCCCTTATCCACGGCCAGGAAC 1339
```

Db 361 GlyProAsnTyrGlnTrpValProTyrGlnGlyArgValProTyrProArgProGlyThr 380
 QY 1340 TGTCAGCAAGCAAAATTTGGTGGTTTGAATCTACAAAGGACCTTCTCTGATGATGTATATA 1399
 Db 381 CysProSerIleThrPheGlyGlyPheAspSerThrIlyAspLeuProAspValIle 400
 QY 1400 ACCTTTGCAGAGAGTATCAGGACATGATACAAATCCAGTGTCTCTATGAACATCCGCCA 1459
 Db 401 ThrPheAlaArgSerHisProAlaMetTyrAsnProValPheProMetAsnAsnArgPro 420
 QY 1460 ATAGTGATCAAAACGGATGAAATTTATCAATTTACACAAATTTCTGAGACCGAGTGGAT 1519
 Db 421 IleValIleThrAspValAsnTyrGlnPheThrGlnIleValValAspArgValAsp 440
 QY 1520 GCAGAGATGCACAGTATGATGTTATGTTATCGAACACAGATGTTGGACCGTCTTAA 1579
 Db 441 AlaGluAspGlyGlnTyrAspValMetPheIleGlyThrAspValGlyThrValLeuLys 460
 QY 1580 GTAGTTTCAATTCCTAAGGAGACTTGATGATTTAGAGAGGTTCTGCTGGAAGAAATG 1639
 Db 461 ValValSerIleProLysGluThrIlePheAspLeuGluValLeuLeuGluMet 480
 QY 1640 ACAGTTTTTCGGGAACCGACTGCTATTTTCAGCAATGAGCTTCCACTAAGCAGCAACA 1699
 Db 481 ThrValPheArgGluProThrAlaIleSerAlaMetGluLeuSerThrLysGlnGln 500
 QY 1700 CTATATATTGTTCAACGGCTGGGGTTGCCAGCTCCCTTTACACCGTGTGATATTAC 1759
 Db 501 LeuTyrIleGlySerThrAlaGlyValAlaGlnLeuProLeuHisArgCysAspIleTyr 520
 QY 1760 GGGAAAGCGTGTGCTGAGTGTGTGCTGCGCCGAGACCTTACTGCTGCTGGGATGGTCT 1819
 Db 521 GlyLysAlaCysAlaGluCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlySer 540
 QY 1820 GCATGTTCTGCTATTTTCCACTGCAAGAGAGCGCACAGACGACAGATATAAGAAAT 1879
 Db 541 AlaCysSerArgTyrPheProThrAlaLysArgArgThrArgArgGlnAspIleArgAsn 560
 QY 1880 GGAGACCCACGACTCAGCTTTCAGCTTACACCATGATATACCATGCGCCACAGCCCT 1939
 Db 561 GlyAspProLeuThrHisCysSerAspLeuHisHisAspAsnHisHisGlyHisSerPro 580
 QY 1940 GAAGAGACATCATCTATGCTGTAGAGAAATAGTAGACATTTTGGAAATCAGTCCGAG 1999
 Db 581 GluGluArgIleIleTyrGlyValGluAsnSerSerThrPheLeuGluCysSerProLys 600
 QY 2000 TCGCAGAGCGCTGCTTATGCAATTCAGAGCGCAATGAAGACGCAAGAAAGAGAG 2059
 Db 601 SerGlnArgAlaLeuValTyrTrpGlnPheGlnArgArgGlnGluArgLysGluGlu 620
 QY 2060 ATCAGAGTGGATGATCATATCATCAGACAGATCAAGCGCTTCTGCTAGCTAGTCTCAA 2119
 Db 621 IleArgValAspAspHisIleArgThrAspGlnGlyLeuLeuLeuLeuArgSerLeuGln 640
 QY 2120 CAGAGGATTCAGCAATTACTCTGCTGCTGCTGCAACATGGTTTCATACAACTCTT 2179
 Db 641 GlnLysAspSerGlyAsnTyrLeuCysHisAlaValGluHisGlyPheIleGlnThrLeu 660
 QY 2180 CTTAAGGTAAACCTGGAAGTCAATTCACACAGAGATTTGGAAGAACTTCTTCATAAAGAT 2239
 Db 661 LeuLysValThrLeuGluValIleAspThrGluHisLeuGluLeuLeuHisLysAsp 680
 QY 2240 GATGATGAGATGGCTCTAAGACCAAGAAATGTCCAATAGCATGACACCTAGCAGAAG 2299
 Db 681 AspAspGlyAspGlySerLysThrLysGluMetSerAsnSerMetThrProSerGlnLys 700
 QY 2300 GTCTGTCACAGAGCTTCATGCTGAGCTCATCAACACACCCCAATCTCAACACGATCGATCAG 2359
 Db 701 ValTrpTyrArgAspPheMetGlnLeuIleAsnHisProAsnLeuAsnThrMetAspGlu 720
 QY 2360 TTCTGTGAACAGTTTGGAAAGGACCGAAACCAACCTCGGCAAGGCGCAGGACATACC 2419
 Db 721 PheCysGluGlnValTrpLysArgAspArgLysGlnArgGlnArgProGlyHisThr 740

QY 2420 CCAGGACACGTACAAATGAGACCTTACAAAGATTAAGAAAGGTAGAAACAGGAGG 2479
 Db 741 ProGlyAsnSerAsnLysTrpLysHisLeuGlnGluAsnLysLysGlyArgAsnArgArg 760
 QY 2480 ACCACCAATTTGAGAGCGCACCCAGGAGTGTCT 2512
 Db 761 ThrHisGluPheGluArgAlaProArgSerVal 771
 RESULT 3
 US-10-067-632-54
 ; Sequence 54, Application US/10067632
 ; Publication No. US20030166849A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Goodman, Corey S.
 ; Kolodkin, Alex L.
 ; Matthes, David
 ; Bentley, David R.
 ; O'Connor, Timothy
 ; TITLE OF INVENTION: The Semaphorin Gene Family
 ; NUMBER OF SEQUENCES: 100
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
 ; STREET: 268 Bush Street, Suite 3200
 ; CITY: San Francisco
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94104
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/067,632
 ; FILING DATE: 04-Feb-2002
 ; CLASSIFICATION: <Unknown>
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/060,610
 ; FILING DATE: <Unknown>
 ; APPLICATION NUMBER: 08/835,268
 ; FILING DATE: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Osman, Richard A.
 ; REGISTRATION NUMBER: 36,627
 ; REFERENCE/DOCKET NUMBER: B94-002-1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415)343-4341
 ; TELEFAX: (415) 343-4342
 ; TELEX: <Unknown>
 ; INFORMATION FOR SEQ ID NO: 54:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 771 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 54:
 ; US-10-067-632-54
 Alignment Scores:
 Pred. No.: 0 Length: 771
 Score: 771.00 Matches: 771
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 86.15% Indels: 0
 DB: 14 Gaps: 0
 US-09-774-490-1 (1-2709) x US-10-067-632-54 (1-771)
 QY 200 ATGGGCTGGTTAACTAGGATTCGTCTCTTCTCGGAGTATTACTTACAGCAAGACA 259
 Db 1 MetGlyTrpLeuThrArgIleValCysLeuPheTrpGlyValLeuLeuThrAlaArgAla 20

QY 260 AACTATCAGATGGGAGAACATGTCGCAAGCTGAATATTCCTACAAAGAAATGTTG 319
 Db |||||
 QY 21 AsnTyrGlnAsnGlyLysAsnAsnValProArgLeuLysLeuSerTyrLysGluMetLeu 40
 Db |||||
 QY 320 GAATCAACAATGATGATCACTTTCAATGGCTTGGCCACACAGCTCCAGTTATCATACCTTC 379
 Db |||||
 QY 41 GluSerAsnAsnValIleThrPheAsnGlyLeuAlaAsnSerSerTyrHisThrPhe 60
 Db |||||
 QY 380 CTTTGGATGAGGACGGAGTAGCTGATGTTGGACAAAGATCAGATATTTTCATC 439
 Db |||||
 QY 61 LeuLeuAspGluGluArgSerArgLeuTyrValGlyAlaLysAspHisIlePheSerPhe 80
 Db |||||
 QY 440 GACCTGGTTAAATCAAGGATTTCAAAAGATGTTGGCCAGTATCTTTACACCAAGAAGA 499
 Db |||||
 QY 81 AspLeuValAsnIleLysAspPheGlnLysIleValTrpProValSerTyrThrArgArg 100
 Db |||||
 QY 500 GATGAATCAAGTGGGCTGGAAAGACATCTCGAAGAAATGTCCTAAATTCATCAAGGTA 559
 Db |||||
 QY 101 AspGluCysLysTrpAlaGlyLysAspIleLeuLysGluCysAlaAsnPheIleLysVal 120
 Db |||||
 QY 560 CTTAAGGCATATAATCAGACTCACTTGATGACGCTGTGGAACGGGGCTTTTCATCCAATT 619
 Db |||||
 QY 121 LeuLysAlaTyrAsnGlnThrHisLeuTyrAlaCysGlyThrGlyAlaPheHisProIle 140
 Db |||||
 QY 620 TGCACCTACATTCAAATTCGACATCATCTGAGGACAATATTTTAAGCTGGAGAACTCA 679
 Db |||||
 QY 141 CysThrTyrIleGluIleGlyHisHisProGluAspAsnIlePheLysLeuGluAsnSer 160
 Db |||||
 QY 680 CATTTTGAAACGGCGTGGAGAGTCCATATGACCTTAAGCTGTCACAGCATCCCTT 739
 Db |||||
 QY 161 HisPheGluAsnGlyArgGlyLysSerProTyrAspProLysLeuLeuThrAlaSerLeu 180
 Db |||||
 QY 740 TTAATAGATGGAGAATTATPACTCTGGAAGTGGAGCTGATTTTATGGGGCGAGCTTTGCT 799
 Db |||||
 QY 181 LeuLeuAspGlyGluLeuTyrSerGlyThrAlaAlaAspPheMetGlyArgAspPheAla 200
 Db |||||
 QY 800 ATCTCCGAACTCTTGGGACACACACCAATCAGGACAGACAGCATGATTCAGGTGG 859
 Db |||||
 QY 201 IlePheArgThrLeuGlyHisHisProIleArgThrGluGlnHisAspSerArgTrp 220
 Db |||||
 QY 860 CTCATATGATCCAAAGTTCAATTAGTGCCACCTCATCTCAGAGAGTGACAATCTCAAGAT 919
 Db |||||
 QY 221 LeuAsnAspProLysPheIleSerAlaHisLeuIleSerGluSerAspAsnProGluAsp 240
 Db |||||
 QY 920 GACAAAGTATATCTTTCTCCGTGAAAATGAAATAGATGGAGAACACTCTCGAAAAGCT 979
 Db |||||
 QY 241 AspLysValTyrPhePhePheArgGluAsnAlaIleAspGlyGluHisSerGlyLysAla 260
 Db |||||
 QY 980 ACTCAGCTAGATAGGTAGATATGCAAGATGCTTTGGAGGACAGAGAGTCTGGTG 1039
 Db |||||
 QY 261 ThrHisAlaArgIleGlyGlnIleCysLysAsnAspPheGlyGlyHisArgSerLeuVal 280
 Db |||||
 QY 1040 AATAAATGACACACATTCCTCAAGCTGCTCTGATTTGCTCAGTCCAGGTCCAATGGC 1099
 Db |||||
 QY 281 AsnLysTrpThrPheLeuLysAlaArgLeuIleCysSerValProGlyProAsnGly 300
 Db |||||
 QY 1100 ATTGACACTCATTTTGAAGAACTGAGAGATGATTCCTTAAGAACTTTAAGATCCTAAA 1159
 Db |||||
 QY 301 IleAspThrHisPheAspGluLeuGlnAspValPheLeuMetAsnPheLysAspProLys 320
 Db |||||
 QY 1160 AATCCAGTTGTATAGGAGTGTATACGACTTCCAGTAAACATTTTCAAGGGATCAGCCGTG 1219
 Db |||||
 QY 321 AsnProValValTyrGlyValPheThrThrSerSerAsnIlePheLysGlySerAlaVal 340
 Db |||||
 QY 1220 TGTATGTATAGATGATGATGAGAGGGTGTTCCTTGGTCCATATGCCACAGGAT 1279
 Db |||||
 QY 341 CysMetTyrSerMetSerAspValArgArgValPheLeuGlyProTyrAlaHisArgAsp 360
 Db |||||
 QY 1280 GGACCCAACTATCAATGGTGGCTTATCAAGAGAGTCCCTATCCACGGCCGAGACT 1339
 Db |||||
 QY 361 GlyProAsnTyrGlnTrpValProTyrGlnGlyArgValProTyrProArgProGlyThr 380
 Db |||||
 QY 1340 TGTCCAGCAAAACATTTGGTGGTTTGACTCTCAAGAGGACCTTCCTGATGATGTATA 1399
 Db |||||

Db 381 CysProSerLysThrPheGlyGlyPheAspSerThrLysAspLeuProAspValIle 400
 QY |||||
 QY 1400 ACCTTTTCAAGAAGTCAATCCAGCCATGATCAATCCAGTGTTCCTATGAACAATCGCCA 1459
 Db |||||
 QY 401 ThrPheAlaArgSerHisProAlaMetTyrAsnProValPheProMetAsnAsnArgPro 420
 Db |||||
 QY 1460 ATAGTGATCAAAACGGATGTAATATTATCAATTTACACAAATGTCGTAGACCGATGGAT 1519
 Db |||||
 QY 421 IleValIleLysThrAspValAsnTyrGlnPheThrGlnIleValValAspArgValAsp 440
 Db |||||
 QY 1520 GCAGAAATGCAGACATGATGATGTTATGTTATCGGAACACAGATGTTGGACCGTCTTAAA 1579
 Db |||||
 QY 441 AlaGluAspGlyGlnTyrAspValMetPheIleGlyThrAspValGlyThrValLeuLys 460
 Db |||||
 QY 1580 GTAGTTTCAATTCCTAAGGACAGCTTGATGATGATTTAGAACAGGTTCTGCGAAGAAATG 1639
 Db |||||
 QY 461 ValValSerIleProLysGluThrTrpTyrAspLeuGluValLeuLeuGluMet 480
 Db |||||
 QY 1640 ACAGTTTTCGGAAACCGACTGCTATTTCAGCAATGGAGCTTTCCACTAAGCAGCAACAA 1699
 Db |||||
 QY 481 ThrValPheArgGluProThrAlaIleSerAlaMetGluLeuSerThrLysGlnGlnGln 500
 Db |||||
 QY 1700 CTATATATTCGTTCAACGGCTGGGTTGCCAGCTCCCTTTTACACCGGTGTGATATTAC 1759
 Db |||||
 QY 501 LeuTyrIleGlySerThrAlaGlyValAlaGlnLeuProLeuHisArgCysAspIleTyr 520
 Db |||||
 QY 1760 GGGAAACGGTGTGCTGAGTGTGCTCGCCGAGAGCCCTTACTGTGCTGGATGGTCTT 1819
 Db |||||
 QY 521 GlyLysAlaCysAlaGluCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlySer 540
 Db |||||
 QY 1820 GCATGTTCTCGCTATTTTCCACTGCAAGAGACGACAGACAGACAGATATAAGAAAT 1879
 Db |||||
 QY 541 AlaCysSerArgTyrPheProThrAlaLysArgArgThrArgGlnAspIleArgAsn 560
 Db |||||
 QY 1880 GGAGACCCACTGACTCACTGTTCCAGACTTACACCATGATTAATCACAATGSCCAGCCCT 1939
 Db |||||
 QY 561 GlyAspProLeuThrHisCysSerAspLeuHisAspAsnHisHisGlyHisSerPro 580
 Db |||||
 QY 1940 GAAGAGAGAAATCATCTATGCTGTAGAGAAATAGTAGCACATTTTGGAAATCCAGTCCGAAG 1999
 Db |||||
 QY 581 GluGluArgIleIleTyrGlyValGluAsnSerSerThrPheLeuGluCysSerProLys 600
 Db |||||
 QY 2000 TCGCAGAGAGCGTGTGCTATTGCGAATTCAGAGCGGAAATGAAGAGCGAAAGAGAG 2059
 Db |||||
 QY 601 SerGlnArgAlaLeuValTyrTrpGlnPheGlnArgAsnGluGluArgLysGluGln 620
 Db |||||
 QY 2060 ATCAGAGTGCATGATCATATCATCAGACAGATCAAGGCTTCTGCTAGTCTCTACAA 2119
 Db |||||
 QY 621 IleArgValAspAspHisIleIleArgThrAspGlnGlyLeuLeuLeuArgSerLeuGln 640
 Db |||||
 QY 2120 CAGAAGGATTCAGGCAATTAACCTCTGCCATGCGGTGGAACATGGTTTCATACAACTCTT 2179
 Db |||||
 QY 641 GlnLysAspSerGlyAsnTyrLeuCysHisAlaValGluHisGlyPheIleGlnThrLeu 660
 Db |||||
 QY 2180 CTTAAGTATACCTCGAAGTCAATGACAGACATTTGGAAGAACTTCTTCAATAGAT 2239
 Db |||||
 QY 661 LeuLysValThrLeuGluValIleAspThrGluHisLeuGluGluLeuLeuHisLysAsp 680
 Db |||||
 QY 2240 GATGATGCAGATGGCTCTTAAGACAAAGAAATGCTCAATAGCATGACACCTAGCCAGAAG 2299
 Db |||||
 QY 681 AspAspGlyAspGlySerLysThrLysGluMetSerAsnSerMetThrProSerGlnLys 700
 Db |||||
 QY 2300 GTCTGTATCAGAGACTTCATGACGTCAATCAACCCCAATCTCAACAGATGGATGAG 2359
 Db |||||
 QY 701 ValTrpTyrArgAspPheMetGlnLeuIleAsnHisProAsnLeuAsnThrMetAspGlu 720
 Db |||||
 QY 2360 TTTCTGTGAACAAGTTTGGAAAAGGGACCGAAAAACAACGCTCGGCAAGGGCCAGCACATACC 2419
 Db |||||
 QY 721 PheCysGluGlnValTrpLysArgAspArgLysGlnArgGlnArgProGlyHisThr 740
 Db |||||
 QY 2420 CCAGGGAAACAGTAACAAATGGAAGCACTTCAAGAAAAATAAGAAAGTGAACAGGAGG 2479
 Db |||||

Db 741 ProGlyAsnSerAsnLysTrpLysHisLeuGlnGluAsnLysGlyArgAsnArgArg 760
 QY 2480 ACCCACGAATTTGAGAGGGACCCAGAGGTGTC 2512
 Db 761 ThrHisGluPheGluArgAlaProArgSerVal 771

RESULT 4
 US-10-247-671-164
 ; Sequence 164, Application US/10247671
 ; Publication No. US20030194721A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mikita, Thomas
 ; APPLICANT: Shiffman, Dov
 ; APPLICANT: Porter, Gordon, J.
 ; APPLICANT: Kaser, Matthew R.
 ; TITLE OF INVENTION: GENES EXPRESSED IN TREATED FOAM CELLS
 ; FILE REFERENCE: PA-0050 US
 ; CURRENT APPLICATION NUMBER: US/10/247,671
 ; CURRENT FILING DATE: 2002-09-18
 ; PRIOR APPLICATION NUMBER: 60/323,784
 ; PRIOR FILING DATE: 2001-09-19
 ; NUMBER OF SEQ ID NOS: 186
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 164
 ; LENGTH: 771
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No. US20030194721A1 1930967CD1
 US-10-247-671-164

Alignment Scores:
 Pred. No.: 0 Length: 771
 Score: 771.00 Matches: 771
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 86.15% Indels: 0
 DB: 14 Gaps: 0

US-09-774-490-1 (1-2709) x US-10-247-671-164 (1-771)

QY 200 ATGGGTGGTTAACTAGGATTCCTGCTCTTTCTGGGAGTATTACTTACAGCAAGACCA 259
 Db 1 Met-GlyTrpLeuThrArgIleValCysLeuPheTrpGlyValLeuLeuThrAlaArgAla 20
 QY 260 AACTATCAGATGGGAGAACAAATGTGCCAGGCTGAATTTATCTCTCAAGAAATCTTG 319
 Db 21 AsnTyrGlnAsnGlyLysAsnValProArgLeuLysLeuSerTyrLysGluMetLeu 40
 QY 320 GAATCCAACTATGATCACTTTCAATGGCTTGGCCACAGCTCCAGTTATCATACCTTC 379
 Db 41 GluSerAsnAsnValIleThrPheAsnGlyLeuAlaAsnSerSerTyrHisThrPhe 60
 QY 380 CTTTGGATCAGAACCGAGTAGCTGTATGTGGAGCAAGATCAATTTTCAATTCATTC 439
 Db 61 LeuLeuAspGluGluArgSerArgLeuTyrValGlyAlaLysAspHisIlePheSerPhe 80
 QY 440 GACCTGGTTAAATCAAGATTTTCAAAAGATTTGTGGCCAGTATCTTACACCAAGA 499
 Db 81 AspLeuValAsnIleLysAspPheGlnLysIleValTrpProValSerTyrThrArgArg 100
 QY 500 GATGAATGCAATGGCTGGAAAGACATCTCTGAAGAAATGTGCTAATTTTCATCAAGTA 559
 Db 101 AspGluCysLysTrpAlaGlyLysAspIleLeuLysGluCysAlaAsnPheIleLysVal 120
 QY 560 CTTAAGGCATATAATCAGACTCACCTGTACCGCTGTGGACGGGGCTTTTCATCCAAAT 619
 Db 121 LeuLysAlaTyrAsnGlnThrHisLeuTyrAlaCysGlyThrGlyAlaPheHisProIle 140
 QY 620 TGCACCTACATTTAAATTTGGACATCATCTCTGAGGACAAATATTTTAACTGGAGACTCA 679
 Db 141 CysThrTyrIleGluIleGlyHisHisProGluAspAsnIlePheLysLeuGluAsnSer 160

QY 680 CATTTTGAACCGCCGTGGGAGAGTCCATATGACCTCAAGCTGCTGACAGCATCCCTT 739
 Db 161 HisPheGluAsnGlyArgGlyLysSerProTyrAspProLysLeuLeuThrAlaSerLeu 180
 QY 740 TTAATAGATGGAGAATTTACTCTGGAACCTGAGCTGATTTTATGGGGCAGAGCTTTGCT 799
 Db 181 LeuIleAspGlyGluLeuTyrSerGlyThrAlaAlaAspPheMetGlyArgAspPheAla 200
 QY 800 ATCTTCCGAACCTCTTGGCCACCACCACCAATCAGGACAGACAGCAGCTATTCAGGTGG 859
 Db 201 IlePheArgThrLeuGlyHisHisHisProIleArgThrGluGlnHisAspSerArgTyr 220
 QY 860 CTCATATGATCCAAAGTTCAATAGTGGCCACCTCATCTCAGAGATGACATCTCTGAAGAT 919
 Db 221 LeuAsnAspProLysPheIleSerAlaHisLeuIleSerGluSerAspAsnProGluAsp 240
 QY 920 GACAAAGTATATCTTTCTTCCTGCGTGAATATCAATAGATGGAGAACACTCTGGAAGCT 979
 Db 241 AspLysValTyrPhePhePheArgGluAsnAlaIleAspGlyGluHisSerGlyLysAla 260
 QY 980 ACTCAGCTAGATAGTTCAGATATGCAAGATGACCTTTGAGGGACACAGAGTCTGGTG 1039
 Db 261 ThrHisAlaArgIleGlyGlnIleCysLysAsnAspPheGlyGlyHisArgSerLeuVal 280
 QY 1040 AATAAATGACAACTTCTCTCAAGCTCGTCTGATTTGCTCAGTCCAGCTCCAAATGGC 1099
 Db 281 AsnLysTrpThrPheLeuLysAlaArgLeuIleCysSerValProGlyProAsnGly 300
 QY 1100 ATTGACACTCATTTTGTATGAACTGAGAGTATCTTAATGAACTTTAAGATTCCTAAA 1159
 Db 301 IleAspThrHisPheAspGluLeuGlnAspValPheLeuMetAsnPheLysAspProLys 320
 QY 1160 AATCCAGTTGTATATGAGTCTTTACGACTTCCAGTAAACATTTTCAAGGATCAGCCGTG 1219
 Db 321 AsnProValValTyrGlyValPheThrSerSerAsnIlePheLysGlySerAlaVal 340
 QY 1220 TGTATGTATAGATGAGTATGAGAGGGTGTCTTGTGTCATATGCCCCACAGGAT 1279
 Db 341 CysMetTyrSerMetSerAspValArgValPheLeuGlyProTyrAlaHisArgAsp 360
 QY 1280 GGACCCCACTCAATGGTGGCTTATCAAGGAGAGTCCCTTATCACGCCGAGCAACT 1339
 Db 361 GlyProAsnTyrGlnTrpValProTyrGlnGlyArgValProTyrProArgProGlyThr 380
 QY 1340 TGTCCCAACAAACATTTGGTGGTTTGACTCTCAAAAGGACCTTCTCTGATGATGTATA 1399
 Db 381 CysProSerLysThrPheGlyGlyPheAspSerThrLysAspLeuProAspAspValIle 400
 QY 1400 ACCTTTGCACAAAGTCAATCCAGCCATGTACAATCCAGTGTTCCTATGAACATTCGCCCA 1459
 Db 401 ThrPheAlaArgSerHisProAlaMetTyrAsnProValPheProMetAsnAsnArgPro 420
 QY 1460 ATAGTGAATCAAAACGGATGTAATTAATCAATTTACAAATTTCTGTAGACCGAGTGGAT 1519
 Db 421 IleValIleLysThrAspValAsnTyrGlnPheThrGlnIleValValAspArgValAsp 440
 QY 1520 GCAGAGATGACAGATGATGTATGTATCGGAACAGATGTGCGGACCGTCTCTTAAA 1579
 Db 441 AlaGluAspGlyGlnTyrAspValMetPheIleGlyThrAspValGlyThrValLeuLys 460
 QY 1580 GTAGTTTCAATTCCTTAGGAGACTTGTGTATGATTTAGAGAGGTTCTCTCTGGAAGAAATG 1639
 Db 461 ValValSerIleProLysGluThrTyrTyrAspLeuGluValLeuLeuGluMet 480
 QY 1640 ACAGTTTTCGGGAACCGACTGTCTATTTCAGCAATGAGCTTTCCTCACTAAGCAGCAACA 1699
 Db 481 ThrValPheArgGluProThrAlaIleSerAlaMetGluLeuSerThrLysGlnGln 500
 QY 1700 CTATATATTTGGTCAACGGCTGGGGTTGCCAGCTCCCTTTACACCGGTGTGATATTAC 1759
 Db 501 LeuTyrIleGlySerThrAlaGlyValAlaGlnLeuProLeuHisArgCysAspIleTyr 520

```
QY 1760 GGGAAAGCGTGTGAGTGTGCTCGCCCGGAGACCCCTTACTGTGCTTGGATGTTCT 1819
Db 521 GlyLysAlaCysAlaGluCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlySer 540
QY 1820 GCATGTTCTCGGTATTTTCCCACTGCAAGACACGACCAAGACGACGATATAAGAAAT 1879
Db 541 AlaCysSerArgTyrPheProThrAlaLysArgThrArgArgGlnAspIleArgAsn 560
QY 1880 GGAGACCCACTGACTCAGTCTTCCAGCTTACACCATGATTAATCACCATGGCCACAGCCCT 1939
Db 561 GlyAspProLeuThrHisCysSerAspLeuHisHisAspAsnHisHisGlyHisSerPro 580
QY 1940 GAAGAGAGAAATCATCTATGCTGTAGAGATAGTACACATTTTTCGAAATGAGTCCGAG 1999
Db 581 GluGluArgIleIleTyrGlyValGluAsnSerSerThrPheLeuGluCysSerProLys 600
QY 2000 TCCGAGAGAGCCCTCGTCTATTGGCAATTCAGAGCGGCAATGAAGAGCGAAAGAGAG 2059
Db 601 SerGlnArgAlaLeuValTyrTrpGlnPheGlnArgArgAsnGluGluArgLysGluGlu 620
QY 2060 ATCAGAGTGGATGATCATATCATCAGGACAGATCAAGGCCCTTCTGCTAGTACTACAA 2119
Db 621 IleArgValAspAspHisIleIleArgThrArgGlnGlyLeuLeuLeuArgSerLeuGln 640
QY 2120 CAGAAGGATTCAGGCAATTACCTCTGCCATGCGGTGGAAACATGGGTTTCATACAACTCT 2179
Db 641 GlnLysAspSerGlyAsnTyrLeuCysHisAlaValGluHisGlyPheIleGlnThrLeu 660
QY 2180 CTTAAGGTAAACCTCGAAGTCAATTGACACAGAGCATTTGGAGAACTTCTTCATAAAGAT 2239
Db 661 LeuLysValThrLeuGluValIleAspThrGluHisLeuGluGluLeuLeuHisLysAsp 680
QY 2240 GATGATGAGATGGCTCTAAGACCAAGAAATGTCCATAGCATGACACCTAGCCAGAG 2299
Db 681 AspAspGlyAspGlySerLysThrLysGluMetSerAsnSerMetThrProSerGlnLys 700
QY 2300 GTCTCGTACAGAGATTCATGAGCTCATCAACACCCCAATCTCAACACCATGGATGAG 2359
Db 701 ValTrpTyrArgAspPheMetGlnLeuIleAsnHisProAsnLeuAsnThrMetAspGlu 720
QY 2360 TTCTCTGACAGAGTTTGAAGAGGACCGCAACACACCTCGCGAAAGCCGAGCATACC 2419
Db 721 PheCysGluGlnValTrpLysArgAspArgLysGlnArgGlnArgProGlyHisThr 740
QY 2420 CCAGGGAACAGTAAACAAATGAAGCACTTACAAGAAAAATAAGAAAGTAGAAACAGGAGG 2479
Db 741 ProGlyAsnSerAsnLysTrpLysHisLeuGlnGluAsnLysLysGlyArgAsnArgArg 760
QY 2480 ACCCAGCAATTGACAGGCGCCACCCAGGAGTGT 2512
Db 761 ThrHisGluPheGluArgAlaProArgSerVal 771

RESULT 5
US-10-320-769-3
; Sequence 3, Application US/10320769
; Publication No. US20030158402A1
; GENERAL INFORMATION:
; APPLICANT: HALL, Kathryn T.
; APPLICANT: FREEMAN, Gordon J.
; APPLICANT: SCHULTZE, Joachim L.
; APPLICANT: BOUSSOTIS, Vassiliki
; APPLICANT: NADLER, Lee M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING CD100 MOLECULES
; FILE REFERENCE: DFN-005CPA2,
; CURRENT APPLICATION NUMBER: US/10/320,769
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: US/08/556,422
; PRIOR FILING DATE: 1995-11-09
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 655
; TYPE: PRT
```

ORGANISM: Homo sapiens
US-10-320-769-3

Alignment Scores:

Pred. No.:	0	Length:	655
Score:	655.00	Matches:	655
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	73.18%	Indels:	0
DB:	14	Gaps:	0

US-09-774-490-1 (1-2709) x US-10-320-769-3 (1-655)

```
QY 200 ATGGGCTGTTAACTAGGATTGTCTGCTTTCTGGGAGTATTACTTACGAGCAAGACA 259
Db 1 MetGlyTrpLeuThrArgIleValCysLeuPheTrpGlyValLeuLeuThrAlaArgAla 20
QY 260 AACTATCAGAAATCGGGAAGAAACAATGTCCCAAGCTGAAATTTACCTACAAAGAAATGTTG 319
Db 21 AsnTyrGlnAsnGlnLysAsnAsnValProArgLeuLysLeuSerTyrLysGluMetLeu 40
QY 320 GAATCCAAACAATGTGATCACTTTCAATGGCTTCGCCAAGCTCCAGTTCATCATCCTTC 379
Db 41 GluSerAsnAsnValIleThrPheAsnGlyLeuAlaAsnSerSerSerTyrHisThrPhe 60
QY 380 CTTTTCGATGAGGACGAGTAGCTGTATGTTGGAGCAAGGATCACATATTTTCATTC 439
Db 61 LeuLeuAspGluGluArgSerArgLeuTyrValGlyAlaLysAspHisIlePheSerPhe 80
QY 440 GACCTGTTTAATATCAAGGATTTTCAAAAGATTGTGTGGCCAGTATCTTACACAGAAGA 499
Db 81 AspLeuValAsnIleLysAspPheGlnLysIleValTrpValSerTyrThrArgArg 100
QY 500 GATGAATGCAAGTGGCTGGAAAAGACATCTCGAAAGAAATGCTCTAATTTTCATCAAGTA 559
Db 101 AspGluCysLysTrpAlaGlyLysAspIleLeuLysGluCysAlaAsnPheIleLysVal 120
QY 560 CTTAAGGCATATTAATCAGACTCACTTGTACGCTGTGGAACGGGGCTTTTCATCCAAAT 619
Db 121 LeuLysAlaTyrAsnGlnThrHisLeuTyrAlaCysGlyThrGlyAlaPheHisProIle 140
QY 620 TGCACCTACATTGAATTTGGACATCATCTCTGAGGACAAATATTTTAAAGCTGGAGAACTCA 679
Db 141 CysThrTyrIleGluIleGlyHisHisProGluAspAsnIlePheLysLeuGluAsnSer 160
QY 680 CATTTTGAACCGCGTGGGAAGTCCATATGACCTTAAGCTGTGACAGCATCCCTT 739
Db 161 HisPheGluAsnGlyArgGlyLysSerProTyrAspProLysLeuLeuThrAlaSerLeu 180
QY 740 TTAATAGATGGAGATTTATATCTTGGAACTGCAGCTGATTTTATGGGGCGAGACTTTGCT 799
Db 181 LeuIleAspGlyGluLeuTyrSerGlyThrAlaAlaAspPheMetGlyArgAspPheAla 200
QY 800 ATCTTCGAACTTTGGGACACCAACCAATCAGGACAGAGAGCATGATTCACAGTGG 859
Db 201 IlePheArgThrLeuGlyHisHisHisProIleArgThrGluGlnHisAspSerArgTrp 220
QY 860 CTCATATGATCCAAAGTTCAATTAGTGCCACCTCATCTCAGAGAGTGCACAAATCTGAAGAT 919
Db 221 LeuAsnAspProLysPheIleSerAlaHisLeuIleSerGluSerAspAsnProGluAsp 240
QY 920 GACAAAGTATACCTTTTCTTCGTTGAAAATGCAATAGATGGAGAACACTCTCGAAAGCT 979
Db 241 AspLysValTyrPhePheArgGluAsnAlaIleAspGlyGluHisSerGlyLysAla 260
QY 980 ACTCAGCTAGATAGTTCAGATATGCAAGATGACTTTTGGAGGGGACAGAGTCTGGTG 1039
Db 261 ThrHisAlaArgIleGlyGlnIleCysLysAsnAspPheGlyGlyHisArgSerLeuVal 280
QY 1040 AATAAATGACACAACTTCCTAAAGCTCTCTGATTGTCTGATTCAGTGCAGGTCCTCAATGCG 1099
Db 281 AsnLysTrpThrThrPheLeuLysAlaArgLeuIleCysSerValProGlyProAsnGly 300
```

QY 1100 ATTGACACTCATTTTGGATGAGTGCAGGATGATTCCTTAATGAACTTTAAAGATCCCTAAA 1159
 Db 301 ILeAspThrHisPheAspGluLeuGlnAspValPheLeuMetAsnPheLysAspProlys 320
 QY 1160 AATCCAGCTGTATATGGAGTGTTCAGACTTCAGTAACATTTTCAAGGGATCAGCGGTG 1219
 Db 321 AsnProValValTyrGlyValPheThrThrSerSerAsnIlePheLysGlySerAlaVal 340
 QY 1220 TGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1279
 Db 341 CysMetTyrSerMetSerAspValArgValPheLeuGlyProTyrAlaHisArgAsp 360
 QY 1280 GGACCAACTATCAATGGGTGCTTATCAAGGAAGTCCCTATCCAGGCCAGGAACT 1339
 Db 361 GlyProAsnTyrGlnTyrValProTyrGlnGlyArgValProTyrProArgProGlyThr 380
 QY 1340 TGTCGAGCAAAACATTTGGTGGTGTTCAGTCTCAAGAGGACCTTCCTGATGATGATGAT 1399
 Db 381 CysProSerLysThrPheGlyGlyPheAspSerThrLysAspLeuProAspValVal 400
 QY 1400 ACCTTTGCAAGAGTTCATCCAGCCATGATCAATCCAGTGTTCCTATCAACAATCGCCCA 1459
 Db 401 ThrPheAlaArgSerHisProAlaMetTyrAsnProValPheProMetAsnAsnArgPro 420
 QY 1460 ATAGTATCAAAACGAGTAAATATCAATTAACAAATGTCGTAGACCGAGTGGAT 1519
 Db 421 IleValIleLysThrAspValAsnTyrGlnPheThrGlnIleValValAspValAsp 440
 QY 1520 GCAGAGATGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1579
 Db 441 AlaGluAspGlyGlnTyrAspValMetPheIleGlyThrAspValGlyThrValLeuLys 460
 QY 1580 GTAGTTTCAATTCCTAAGAGACTTGGTATGATGATGATGATGATGATGATGATGATGATGAT 1639
 Db 461 ValValSerIleProLysGlnTyrTrpTyrAspLeuGluGluValLeuGluMet 480
 QY 1640 ACAGTTTTCGGGACCGACTGCTATTTCCAGCAATGGAGCTTCCACTAAGCAGCAACA 1699
 Db 481 ThrValPheArgGluProThrAlaIleSerAlaMetGluLeuSerThrLysGlnGln 500
 QY 1700 CTATATATTGGTTCAAGCTGGGTGCTCCAGTCTCCCTTACACCGGTGTGATATTAC 1759
 Db 501 LeuTyrIleGlySerThrAlaGlyValAlaGlnLeuProLeuHisArgCysAspIleTyr 520
 QY 1760 GCGAAGAGCTGTGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1819
 Db 521 GlyLysAlaCysAlaGluCysCysLeuAlaArgAspProTyrCysAlaIleTrpAspGlySer 540
 QY 1820 GATGTTCTGCTATTTTCCACTCCAAAGAGACGACACAGACGACAGATATTAAGAAAT 1879
 Db 541 AlaCysSerArgTyrPheProThrAlaLysArgThrArgGlnAspIleArgAsn 560
 QY 1880 GGAGACCCACTGACTCAGTGTTCAGACTTACACCATGATATCACTGAGTCCAGCCAGCCCT 1939
 Db 561 GlyAspProLeuThrHisCysSerAspLeuHisHisAspAsnHisGlyHisSerPro 580
 QY 1940 GAAGAGAGATCATCTATGGTGTAGAGATAGTACACATTTTGGATGATGATGATGATGATGAT 1999
 Db 581 GluGluArgIleIleTyrGlyValGluAsnSerThrPheLeuGluCysSerProLys 600
 QY 2000 TCGCAGAGAGCTGTGCTGCTATTTGGCAATTCAGAGGCGAATGAAGACGCAAGAGAGAG 2059
 Db 601 SerGlnArgAlaLeuValTyrTrpGlnPheGlnArgArgGlnGluArgLysGluGlu 620
 QY 2060 ATCAGAGTGGATGATCATATCATATCATATCATATCATATCATATCATATCATATCATATCAT 2119
 Db 621 IleArgValAspAspHisIleIleArgThrAspGlnGlyLeuLeuLeuLeuArgSerLeuGln 640
 QY 2120 CAGAGAGATTTCAGGCAATTTACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2164
 Db 641 GlnLysAspSerGlyAsnTyrLeuCysHisAlaValGluHisGly 655

US-09-864-761-47112
 ; Sequence 47112, Application US/09864761
 ; Patent No. US20020048761A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Penn, Sharon G.
 ; APPLICANT: Rank, David R.
 ; APPLICANT: Hanzel, David K.
 ; APPLICANT: Chen, Wensheng
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
 ; FILE REFERENCE: Aemica-X-1
 ; CURRENT APPLICATION NUMBER: US/09/864,761
 ; PRIOR FILING DATE: 2001-05-23
 ; PRIOR APPLICATION NUMBER: US 60/180,312
 ; PRIOR FILING DATE: 2000-02-04
 ; PRIOR APPLICATION NUMBER: US 60/207,456
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: US 09/632,366
 ; PRIOR FILING DATE: 2000-08-03
 ; PRIOR APPLICATION NUMBER: GB 24263.6
 ; PRIOR FILING DATE: 2000-10-04
 ; PRIOR APPLICATION NUMBER: US 60/235,359
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: PCT/US01/00666
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00667
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00664
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00669
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00665
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00668
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00663
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00662
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00661
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00670
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: US 60/234,687
 ; PRIOR FILING DATE: 2000-09-21
 ; PRIOR APPLICATION NUMBER: US 09/608,408
 ; PRIOR FILING DATE: 2000-06-30
 ; PRIOR APPLICATION NUMBER: US 09/774,203
 ; PRIOR FILING DATE: 2001-01-29
 ; NUMBER OF SEQ ID NOS: 49117
 ; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
 ; SEQ ID NO 47112
 ; LENGTH: 151
 ; TYPE: PRX
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: MAP TO AC006322.2
 ; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.73
 ; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.55
 ; OTHER INFORMATION: SWISSPROT HIT: Q14563, EVALUE 2.00e-88
 US-09-864-761-47112
 Alignment Scores:
 Pred. No.: 5,29e-138 Length: 151
 Score: 151.00 Matches: 151
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 16.87% Indels: 0
 DB: 9 Gaps: 0
 US-09-774-490-1 (1-2709) x US-09-864-761-47112 (1-151)
 QY 2060 ATCAGAGTGGATGATCATATCATATCATATCATATCATATCATATCATATCATATCATATCAT 2119

1	IleArgValAspAspHisIleIleArgThrAspGlnGlyLeuLeuLeuArgSerLeuGln	20
2120	CAGAAGATTTCAGGCAAATTACCTCTCCATCGCGTGGAAACATGGGTTCATACAAACTCTT	2179
21	GlnLysAspSerGlyAsnTyLeuCysHisAlaValGluHisGlyPheIleGlnThrLeu	40
2180	CTTAAGGTAAACCTCGAAGTCATTGCACACAGACATTTGGAAGAACTTCTTCATAAGAT	2239
41	LeuLysValThrLeuGluValIleAspThrGluHisLeuGluGluLeuLeuHisLysAsp	60
2240	GATGATGGAGATGGCTCTAAGACCAAGAATAATGCCAATAGCATGACACCTAGCCAGAAG	2299
61	AspAspGlyAspGlySerLysThrLysGluMetSerAsnSerMetThrProSerGlnLys	80
2300	GNCTGCTACAGACACTCATGACAGCTCATCAACACCCCAATCTCAACAGATGGATGAG	2359
81	ValTrpTyArgAspPheMetGlnLeuIleAsnHisProAsnLeuAsnThrMetAspGlu	100
2360	TTCTGTGAACAAGTTTGGAAAAGGGACCGAAAAACAACGTCGGCAAGGCCAGACACATACC	2419
101	PheCysGluGlnValTrpLysArgAspArgLysGlnArgGlnArgProGlyHisThr	120
2420	CCAGGGAACAGTTAACAAATGGAAAGCACTTACAGAAATAAGAAAGTAGAAACAGGAGG	2479
121	ProGlyAsnSerAsnLysTrpLysHisLeuGlnGluAsnLysLysGlyArgAsnArgArg	140
2480	ACCACGAAATTGAGAGGGCACCCAGGATGTC	2512
141	ThrHisGluPheGluArgAlaProArgSerVal	151

RESULT 7

```

US-09-773-876-5
; Sequence 5, Application US/09773876
; Publication, NO: US2002003993A1
; GENERAL INFORMATION:
; APPLICANT: Winchester, Robert J.
; APPLICANT: Seki, Tetsunori
; APPLICANT: Guiko, Percio Saltz
; TITLE OF INVENTION: USE OF INHIBITORS OF CXCR4 RECEPTOR BY SDF-1 IN
; TREATING RHEUMATOID ARTHRITIS
; FILE REFERENCE: 0575/57005-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/773,876
; CURRENT FILING DATE: 2001-01-31
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-773-876-5

```

Alignment Scores:	4.06e-88	Length:	100
Pred. No.:	100.00	Matches:	100
Score:	100.00	Conservative:	0
Percent Similarity:	100.00%	Mismatches:	0
Best Local Similarity:	100.00%	Indels:	0
Query Match:	11.17%	Gaps:	0
DB:	12		

US-09-774-490-1 (1-2709) x US-09-773-876-5 (1-100)

1211	TCACCCGCTGTATGATATACATCAGTGGATGTCAGAAAGGCTGCTCTGGTCCATATGCC	QY	1270
	1 SerAlaValCysMetIysSerMetSerAspValArgValPheLeuGlyProTyrAla	Db	20
1271	CACAGGGATGGACCCCAACTATCAATGGTGCCTTATCAAGAAAGGTCCTCCATCCACGG	QY	1330
	21 HisArgAspGlyProAsnTyrGlnTrpValProTyrGlnGlyArgValProTyrProArg	Db	40
1331	CCAGGAACCTGTGCCAGCAAAACATTTGGTGGTTTTCACCTCTCAAAAGGACCTTCCTGAT	QY	1390
	41 ProGlyThrCysProSerLysThrPheGlyGlyPheAspSerThrLysAspLeuProAsp	Db	60

```

QY      1391  GATGTTATACCTTTGCAGAAGTCATCCAGCCATGTACAATCCAGTGTTCCTATGAAC 1450
DB      61  AspValIleThrPheAlaArgSerHisProAlaMetTyrAsnProValPheProMetAsn 80
QY      1451  AATCGCCCAATAGTCATCAAAACGGATGTAATATTCATTAATTACACAAATTTGCTAGTAC 1510
DB      81  AsnArgProIleValIleAlaIleLysThrAspValAsnTyrGlnPheThrGlnIleValValAsp 100

RESULT 8
US-10-029-386-30748
; Sequence 30748, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USED
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Anncmax Sequence Listing Engine vers. 1.1
; SEQ ID NO 30748
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR7.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.59
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.4
; OTHER INFORMATION: SWISSPROT HIT: Q14563, EVALUAE 8.00e-29
US-10-029-386-30748

```

Alignment Scores:

Programme Scores:	
Score, No.1	54
Score, No.2	54
Length:	54
Matches:	54
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0
DB:	14
US-09-774-490-1 (1-2709) x US-10-029-386-30748 (1-54)	

UIS-09-274-490-1 (1-2709) x UIS-10-029-386-30748 (1-54)

QY	1691	CAGCAACAACACTATATTGGTTTCAACGCGTGCGGGTGCACCTCCCTTTACACCGGTG	1750
DB	1	GinGlnClnLeuTyrlleGlySerThrAlaGlyValAlaGlnLeuProIeuHisArgCys	20
QY	1751	GATATTTACGGGAACGCGTGCTCAGTGTTCCCTGCCGCGAGACCTTACTGTGCTGG	1810
DB	21	AspIleTyrglyAlaCysalagluCysCysLeuAlaArgAspProTyrCysalaTrp	40
QY	1811	GATGGTTTCGCATGTCTCGCTATTTTCCCACCTGCAAGAGA	1852
DB	41	AsnGlySerAlaCysSerArgTrpPheProThrAlaLysArg	54

RESULT 9

```

US-09-864-761-44075
; Sequence 44075, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23

```

; PRIOR APPLICATION NUMBER: US 60/180,312
 ; PRIOR FILING DATE: 2000-02-04
 ; PRIOR APPLICATION NUMBER: US 60/207,456
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: US 09/632,366
 ; PRIOR FILING DATE: 2000-08-03
 ; PRIOR APPLICATION NUMBER: GB 24263.6
 ; PRIOR FILING DATE: 2000-10-04
 ; PRIOR APPLICATION NUMBER: US 60/236,359
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: PCT/US01/00666
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00667
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00664
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00669
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00665
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00668
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00663
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00662
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00661
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00670
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: US 60/234,687
 ; PRIOR FILING DATE: 2000-09-21
 ; PRIOR APPLICATION NUMBER: US 09/608,408
 ; PRIOR FILING DATE: 2000-06-30
 ; PRIOR APPLICATION NUMBER: US 09/774,203
 ; PRIOR FILING DATE: 2001-01-29
 ; NUMBER OF SEQ ID NOS: 49117
 ; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
 ; SEQ ID NO 44075
 ; LENGTH: 57
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: MAP TO AC004848.1
 ; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2
 ; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1
 ; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.3
 ; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
 ; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2
 ; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2
 ; OTHER INFORMATION: SWISSPROT HIT: Q14563, EVALUATION 5.00e-25
 ; US-09-774-490-1 (1-2709) x US-09-864-761-44075

Alignment Scores:
 Pred. No.: 3,9e-42 Length: 57
 Score: 53.00 Matches: 53
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 5.92% Indels: 0
 DB: 9 Gaps: 0

US-09-774-490-1 (1-2709) x US-09-864-761-44075 (1-57)

QY 311 GAAATGTTGGAATCCAAATGTGATCATTTCATCGCTGGCCAAAGTCAGTTAT 370
 Db 5 GluMetLeuGluSerAsnValIleThrPheAsnGlyLeuAlaAsnSerSerTyr 24
 QY 371 CATACCTTCCTTTGGATGAGCAAGGAGTAGGCTGTATGTTGGAGCAAGATCACATA 430
 Db 25 HisThrPheLeuLeuAspGluArgSerArgLeuTyrValGlyAlaLysAspHisIle 44
 QY 431 TTTTCATTCCGACCTGGTTAATATCAAGGATTTTCAAAAG 469

Db 45 PheSerPheAspLeuValAsnIleLysAspPheGlnLys 57

RESULT 10
 US-10-029-386-29372
 ; Sequence 29372, Application US/10029386
 ; Publication No. US20030194704A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Penn, Sharon G.
 ; APPLICANT: Rank, David R.
 ; APPLICANT: Hanzel, David K.
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR C
 ; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
 ; FILE REFERENCE: AEMICA-X-2
 ; CURRENT APPLICATION NUMBER: US/10/029,386
 ; CURRENT FILING DATE: 2001-12-20
 ; NUMBER OF SEQ ID NOS: 34288
 ; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
 ; SEQ ID NO 29372
 ; LENGTH: 60
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: MAP TO CHR7.1
 ; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.5
 ; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.68
 ; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.64
 ; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.7
 ; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.69
 ; OTHER INFORMATION: SWISSPROT HIT: Q14563, EVALUATION 5.00e-25
 ; US-10-029-386-29372

Alignment Scores:
 Pred. No.: 3,88e-42 Length: 60
 Score: 53.00 Matches: 53
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 5.92% Indels: 0
 DB: 14 Gaps: 0

US-09-774-490-1 (1-2709) x US-10-029-386-29372 (1-60)

QY 311 GAAATGTTGGAATCCAAATGTGATCATTTCATCGCTGGCCAAAGTCAGTTAT 370
 Db 4 GluMetLeuGluSerAsnValIleThrPheAsnGlyLeuAlaAsnSerSerTyr 23
 QY 371 CATACCTTCCTTTGGATGAGCAAGGAGTAGGCTGTATGTTGGAGCAAGATCACATA 430
 Db 24 HisThrPheLeuLeuAspGluArgSerArgLeuTyrValGlyAlaLysAspHisIle 43
 QY 431 TTTTCATTCCGACCTGGTTAATATCAAGGATTTTCAAAAG 469
 Db 44 PheSerPheAspLeuValAsnIleLysAspPheGlnLys 56

RESULT 11
 US-09-864-761-44552
 ; Sequence 44552, Application US/09864761
 ; Patent No. US20020048763A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Penn, Sharon G.
 ; APPLICANT: Rank, David R.
 ; APPLICANT: Hanzel, David K.
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
 ; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
 ; FILE REFERENCE: Aemica-X-1
 ; CURRENT APPLICATION NUMBER: US/09/864,761
 ; CURRENT FILING DATE: 2001-05-23
 ; PRIOR APPLICATION NUMBER: US 60/180,312
 ; PRIOR FILING DATE: 2000-02-04
 ; PRIOR APPLICATION NUMBER: US 60/207,456
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: US 09/632,366
 ; PRIOR FILING DATE: 2000-08-03

;; PRIOR APPLICATION NUMBER: GB 24263.6
;; PRIOR FILING DATE: 2000-10-04
;; PRIOR APPLICATION NUMBER: US 60/236,359
;; PRIOR FILING DATE: 2000-09-27
;; PRIOR APPLICATION NUMBER: PCT/US01/00666
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00667
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00664
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00669
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00665
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00668
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00663
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00662
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00661
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00670
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: US 60/234,687
;; PRIOR FILING DATE: 2000-09-21
;; PRIOR APPLICATION NUMBER: US 09/608,408
;; PRIOR FILING DATE: 2000-06-30
;; PRIOR APPLICATION NUMBER: US 09/774,203
;; PRIOR FILING DATE: 2001-01-29
;; NUMBER OF SEQ ID NOS: 49117
;; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
;; SEQ ID NO 44552
;; LENGTH: 41
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: MAP TO AC006322.2
;; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.46
;; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.54
;; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.56
;; OTHER INFORMATION: EST HUMAN HIT: BF700780.1, EVALUATE 1.00e-17
;; OTHER INFORMATION: SWISSPROT HIT: Q14563, EVALUATE 1.00e-18

US-09-774-490-1 (1-2709) x US-09-864-761-44552 (1-41)

Alignment Scores:
Pred. No.: 2,2e-30 Length: 41
Score: 41.00 Matches: 41
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.58% Indels: 0
DB: 9 Gaps: 0

US-09-774-490-1 (1-2709) x US-09-864-761-44552 (1-41)

QY 1937 CTTGACAGACATATCTATGCTAGAGATAGACACATTTTGGATGACGTCG 1996
|||
Db 1 ProGluGluArgIleTyrGlyValGluAsnSerSerThrPheLeuGluCysSerPro 20
|||
QY 1997 AAGTCGACAGAGCGTGTGCTATTGGCAATTCACAGCGCGAAATGAAGAGCGAAAGAA 2056
|||
Db 21 LysSerGlnArgAlaLeuValTyrTrpGlnPheGlnArgGAsnGluGluArgGlySgu 40
|||

QY 2057 GAG 2059

Db 41 Glu 41

RESULT 12

US-09-864-761-39708
; Sequence 39708, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.

;; APPLICANT: Rank, David R.
;; APPLICANT: Hanzel, David K.
;; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;; FILE REFERENCE: Aecomica-X-1
;; CURRENT APPLICATION NUMBER: US/09/864,761
;; CURRENT FILING DATE: 2001-05-23
;; PRIOR APPLICATION NUMBER: US 60/180,312
;; PRIOR FILING DATE: 2000-02-04
;; PRIOR APPLICATION NUMBER: US 60/207,456
;; PRIOR FILING DATE: 2000-05-26
;; PRIOR APPLICATION NUMBER: US 09/632,366
;; PRIOR FILING DATE: 2000-08-03
;; PRIOR APPLICATION NUMBER: GB 24263.6
;; PRIOR FILING DATE: 2000-10-04
;; PRIOR APPLICATION NUMBER: US 60/236,359
;; PRIOR FILING DATE: 2000-09-27
;; PRIOR APPLICATION NUMBER: PCT/US01/00666
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00667
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00664
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00669
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00665
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00668
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00663
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00662
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00661
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00670
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: US 60/234,687
;; PRIOR FILING DATE: 2000-09-21
;; PRIOR APPLICATION NUMBER: US 09/608,408
;; PRIOR FILING DATE: 2000-06-30
;; PRIOR APPLICATION NUMBER: US 09/774,203
;; PRIOR FILING DATE: 2001-01-29
;; NUMBER OF SEQ ID NOS: 49117
;; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
;; SEQ ID NO 39708
;; LENGTH: 33
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: MAP TO AC004848.1
;; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.5
;; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.5
;; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.5
;; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.7
;; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.5
;; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.6
;; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.5
;; OTHER INFORMATION: SWISSPROT HIT: Q14563, EVALUATE 4.00e-15

US-09-864-761-39708

Alignment Scores:

Pred. No.: 1.5e-22 Length: 33
Score: 33.00 Matches: 33
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.69% Indels: 0
DB: 9 Gaps: 0

US-09-774-490-1 (1-2709) x US-09-864-761-39708 (1-33)

QY 533 AAAGAATGCTAATTTTCATCAAGGTACTTAAGGCATATAATCAGACTCACTTGTCGCC 552

Db 1 LysGluCysAlaAsnPhelIleLysValLeuLysAlaTyrAsnGlnThrHisLeuTyrAla 20

Qy 593 TGTGAACGGGGGCTTTTCATCCAAATTCACCTACATT 631

Db 21 CysGlyThrGlyAlaPheHisProileCysThrTyrile 33

RESULT 13

US-09-731-179-2
; Sequence 2, Application US/09731179
; Patent No. US20010049432A1
; GENERAL INFORMATION:
; APPLICANT: Holloway, James L..
; APPLICANT: Foley, Kevin P..
; TITLE OF INVENTION: HUMAN SEMAPHORIN ZSMF-16
; FILE REFERENCE: 99-90
; CURRENT APPLICATION NUMBER: US/09/731,179
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: US 60/169,238
; PRIOR FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 779
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-731-179-2

Alignment Scores:
Pred. No.: 4,42e-07 Length: 779
Score: 17.00 Matches: 17
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.90% Indels: 0
Gaps: 0

US-09-774-490-1 (1-2709) x US-09-731-179-2 (1-779)

Qy 1766 GCGTGTGCTGAGTGTGCTCCCGAGACCTTACTGTGCTGGGATGGT 1816
Db 525 AlaCysAlaGluCysCysLeuAlaArgAspProTyrCysAlaTrpAspGly 541

RESULT 14

US-09-813-290-4
; Sequence 4, Application US/09813290
; Patent No. US20020042504A1
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wilganowski, Nathaniel L..
; APPLICANT: Hilbun, Erin
; APPLICANT: Turner, C. Alexander Jr..
; APPLICANT: Wang, Xiaoming
; APPLICANT: Donoho, Gregory
; TITLE OF INVENTION: No. US20020042504A1 Human Secreted Proteins and Polynucleotides
; FILE REFERENCE: LEX-0151-USA
; CURRENT APPLICATION NUMBER: US/09/813,290
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/190,638
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 60/191,188
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: US 60/193,639
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 782
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-813-290-4

Alignment Scores:

Pred. No.: 4,42e-07 Length: 782
Score: 17.00 Matches: 17
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.90% Indels: 0
Gaps: 0

US-09-774-490-1 (1-2709) x US-09-813-290-4 (1-782)

Qy 1766 GCGTGTGCTGAGTGTGCTCCCGAGACCTTACTGTGCTGGGATGGT 1816
Db 528 AlaCysAlaGluCysCysLeuAlaArgAspProTyrCysAlaTrpAspGly 544

RESULT 15

US-09-813-290-2
; Sequence 2, Application US/09813290
; Patent No. US20020042504A1
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wilganowski, Nathaniel L..
; APPLICANT: Turner, C. Alexander Jr..
; APPLICANT: Hilbun, Erin
; APPLICANT: Wang, Xiaoming
; APPLICANT: Donoho, Gregory
; TITLE OF INVENTION: No. US20020042504A1 Human Secreted Proteins and Polynucleotides
; FILE REFERENCE: LEX-0151-USA
; CURRENT APPLICATION NUMBER: US/09/813,290
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/190,638
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 60/191,188
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: US 60/193,639
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 875
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-813-290-2

Alignment Scores:

Pred. No.: 4,35e-07 Length: 875
Score: 17.00 Matches: 17
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.90% Indels: 0
Gaps: 0

US-09-774-490-1 (1-2709) x US-09-813-290-2 (1-875)

Qy 1766 GCGTGTGCTGAGTGTGCTCCCGAGACCTTACTGTGCTGGGATGGT 1816
Db 621 AlaCysAlaGluCysCysLeuAlaArgAspProTyrCysAlaTrpAspGly 637

Search completed: September 21, 2004, 21:18:30

Job time : 343 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: September 21, 2004, 19:47:54 ; Search time 53.5 Seconds
(without alignments)
5228.215 Million cell updates/sec

Title: US-09-774-490-1

Perfect score: 895
Sequence: 1 aatctttttttatcgatg.....agggtttttttcttaataacc 2709

Scoring table:

OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 389414 seqs, 51625971 residues

Word size: 1

Total number of hits satisfying chosen parameters: 663654

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

-MODEL=frame-n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO.spool.p/US09774490/runat_21092004_144321_2615/app_query.fasta_1.2887
-DB=Issued Patents AA -QFMT=fastan -SUFFIX=oligo.ra1 -MINMATCH=0.1 -LOOPEL=0
-LOOPEXT=0 -UNITS=bits -SPART=1 -END=1 -MATRIX=oligo -TRANS=humar40.cdi
-LIST=45 -DOCALIGN=200 -THE SCORE=quality -THR_MIN=3 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09774490@cgn_1_1_74 @runat_21092004_144321_2615 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPEL=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=60
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : Issued Patents AA.*

1: /cgn2_6/ptodata/2/iaa/5A.COMB.pcp.*
2: /cgn2_6/ptodata/2/iaa/5B.COMB.pcp.*
3: /cgn2_6/ptodata/2/iaa/6A.COMB.pcp.*
4: /cgn2_6/ptodata/2/iaa/6B.COMB.pcp.*
5: /cgn2_6/ptodata/2/iaa/PTUS.COMB.pcp.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	771	86.1	771	1	US-08-121-713D-54
2	771	86.1	771	1	US-08-835-268-54
3	771	86.1	771	2	US-09-060-692-54
4	771	86.1	771	3	US-08-833-391-54
5	771	86.1	771	4	US-09-060-610-54
6	771	86.1	771	5	US-09-060-610-54
7	655	73.2	655	4	US-08-556-422A-3
8	434	48.5	477	1	US-08-136-922-2
9	13	1.5	775	4	US-09-308-179B-1
10	10	1.1	606	3	US-09-041-236-4
11	10	1.1	606	4	US-09-771-467C-4
12	9	1.0	112	4	US-09-341-461-34
C	12	9	1.0	4	US-09-341-461-34

13	9	1.0	295	4	US-08-556-422A-6	Sequence 6, Appli
14	9	1.0	425	4	US-08-556-422A-7	Sequence 7, Appli
15	9	1.0	607	4	US-08-556-422A-4	Sequence 4, Appli
16	9	1.0	690	4	US-09-252-991A-32350	Sequence 2350, A
17	9	1.0	862	4	US-08-556-422A-2	Sequence 2, Appli
18	9	1.0	913	4	US-08-971-089-4	Sequence 4, Appli
19	8	0.9	57	4	US-09-152-060-58	Sequence 58, Appli
20	8	0.9	139	4	US-09-252-991A-24681	Sequence 24681, A
21	8	0.9	332	4	US-09-252-991A-32158	Sequence 32158, A
22	8	0.9	360	4	US-09-252-991A-20193	Sequence 20193, A
23	8	0.9	374	1	US-08-464-148-2	Sequence 2, Appli
24	8	0.9	374	1	US-08-385-500-2	Sequence 2, Appli
25	8	0.9	374	1	US-08-846-784-2	Sequence 2, Appli
26	8	0.9	454	3	US-09-080-044-4	Sequence 4, Appli
27	8	0.9	454	4	US-09-531-857A-4	Sequence 4, Appli
28	8	0.9	673	4	US-09-252-991A-25962	Sequence 25962, A
29	8	0.9	849	4	US-09-157-257-4	Sequence 4, Appli
30	7	0.8	17	1	US-08-644-456-1	Sequence 1, Appli
31	7	0.8	28	1	US-08-164-151-22	Sequence 22, Appli
32	7	0.8	37	4	US-09-574-377-27	Sequence 27, Appli
33	7	0.8	43	4	US-09-205-258-296	Sequence 296, App
34	7	0.8	46	4	US-09-369-247-82	Sequence 82, Appli
35	7	0.8	48	4	US-09-489-847-175	Sequence 175, App
36	7	0.8	49	4	US-09-716-129-71	Sequence 71, Appli
37	7	0.8	62	4	US-08-328-352-7261	Sequence 7261, Ap
38	7	0.8	62	4	US-09-621-976-6807	Sequence 6807, Ap
39	7	0.8	62	6	5320958-24	Patent No. 5320958
40	7	0.8	67	4	US-09-107-532A-4497	Sequence 4497, Ap
41	7	0.8	68	2	US-08-456-647B-31	Sequence 31, Appli
42	7	0.8	68	2	US-08-237-401A-31	Sequence 31, Appli
43	7	0.8	69	4	US-09-134-001C-5401	Sequence 5401, Ap
44	7	0.8	70	4	US-09-621-976-5508	Sequence 5508, Ap
45	7	0.8	70	4	US-09-621-976-5563	Sequence 5563, Ap

ALIGNMENTS

RESULT 1
US-08-121-713D-54
; Sequence 54, Application US/08121713D
; Patent No. 5639856
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey S.
; APPLICANT: Kolodkin, Alex L.
; APPLICANT: Matthes, David
; APPLICANT: Bentley, David R.
; APPLICANT: O'Connor, Timothy
; TITLE OF INVENTION: The Semaphorin Gene Family
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 Bush Street, Suite 3200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/121,713D
; FILING DATE: 13-SEP-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B94-002-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; TELEX:

; INFORMATION FOR SEQ ID NO: 54:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 771 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-121-713D-54

Alignment Scores:

Pred. No.:	0	Length:	771
Score:	771.00	Matches:	771
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	86.15%	Indels:	0
DB:	1	Gaps:	0

US-09-774-490-1 (1-2709) x US-08-121-713D-54 (1-771)

QY	200	ATGGCGTGGTAACTAGGATTGCTGCTTTCTGGGGAGTATTACTTACAGCAAGAGCA	259
Db	1	MetGlyTrpLeuThrArgIleValCysLeuPheTrpGlyValLeuLeuThrAlaArgAla	20
QY	260	AACTATCAGATGGGAAGCAAACTGCCAAGGCTGAAATTTATCTCAAAAGAAATGTG	319
Db	21	AsnTyrGlnAsnGlyLysAsnValProArgLeuLysLeuSerTyrLysGluMetLeu	40
QY	320	GAATCCAAATGATCACTTTCAATGGCTGGCCAAAGCTCCAGCTTATCATCTTC	379
Db	41	GluSerAsnAsnValIleThrPheAsnGlyLeuAlaAsnSerSerTyrHisThrPhe	60
QY	380	CTTTTGGATGAGAACCGAGTAGCTGTATGTCGAGCAAGGATCATATTTTCAATC	439
Db	61	LeuLeuAspGluGluArgSerArgLeuTyrValGlyAlaLysAspHisIlePheSerPhe	80
QY	440	CACCTGGTTAATATCAAGGATTTTCAAAGATTGTGGCCAGTATCTTACACAGAGA	499
Db	81	AspLeuValAsnIleLysAspPheGlnLysIleValTrpProValSerTyrThrArgArg	100
QY	500	GATGATCAAGTGGCTGGAAAGACATCTGTAAGAAATGTGCTAATTTTCATCAAGTA	559
Db	101	AspGluCysLysTrpAlaGlyLysAspLeuLysGluCysAlaAsnPheIleLysVal	120
QY	560	CTTAAGGCATATAATCAGACTCACTGTACGCTGTGGAAAGGGGGCTTTTCATCCAAT	619
Db	121	LeuLysAlaTyrAsnGlnThrHisLeuTyrAlaCysGlyThrGlyAlaPheHisProIle	140
QY	620	TGCACCTACATGAATTTGACATCTCTGAGGACAAATATTTTAAGCTGGAGAACTCA	679
Db	141	CysThrTyrIleGluIleGlyHisHisProGluAspAsnIlePheLysLeuGluAsnSer	160
QY	680	CATTTTGAACCGCGGGAAGAGTCCATATGACCTAAGCTGCTGACAGCATCCCTT	739
Db	161	HisPheGluAsnGlyArgGlySerProTyrAspProLysLeuLeuThrAlaSerLeu	180
QY	740	TTAATAGATGGAATATTACTCTGGAATCCAGCTGATTTTATGGGCGAGACTTTGCT	799
Db	181	LeuIleAspGlyGluLeuTyrSerGlyThrAlaAlaAspPheMetGlyArgAspPheAla	200
QY	800	ATCTTCCGAACCTTTGGCACACCAATCAGGACAGCAGCATGATTCAGAGTGG	859
Db	201	IlePheArgThrLeuGlyHisHisProIleArgThrGluGlnHisAspSerArgTrp	220
QY	860	CTCAATGATCAAAAGTTCATTAGTGGCCACCTCATCTCAGAGAGTGACATCTCGAAGAT	919
Db	221	LeuAsnAspProLysPheIleSerAlaHisLeuIleSerGluSerAspAsnProGluAsp	240
QY	920	GACAAAGTATATTTTCTCCGTGAAATTCGAATAGTAGAGACACTCTCGGAAAAGCT	979
Db	241	AspLysValTyrPhePheArgGluAsnAlaIleAspGlyGluHisSerGlyLysAla	260
QY	980	ACTCACGCTAGAAATAGTCAATATGCAAGATGACATTTGGAGGGCCACAGAGTCTGCTG	1039
Db	261	ThrHisAlaArgIleGlyGlnIleCysLysAsnAspPheGlyGlyHisArgSerLeuVal	280

QY	1040	AATAAATCGAACAAATCTCTCAAGCTGCTGTGATTTGCTCAGTGCAGGTCCAAATGGC	1099
Db	281	AsnLysTrpThrThrPheLeuLysAlaArgLeuIleCysSerValProGlyProAsnGly	300
QY	1100	ATTGACACTCATTTTGTAGTGAACATGACGAGTATTTCTTAATGAACCTTAAAGATCTTAAA	1159
Db	301	IleAspThrHisPheAspGluLeuGlnAspValPheLeuMetAsnPheLysAspProLys	320
QY	1160	AATCCAGTTGTATATGAGTGTATTACGACTTCCAGTAAACATTTCAAGGGATACGCCGTG	1219
Db	321	AsnProValValTyrGlyValPheThrThrSerSerAsnIlePheLysGlySerAlaVal	340
QY	1220	TGTATGTATAGCATGAGTGTGAGAGGGTGTCTTGGTCCATATGCCACAGGAT	1279
Db	341	CysMetTyrSerMetSerAspValArgArgValPheLeuGlyProTyrAlaHisArgAsp	360
QY	1280	GGACCAACTATCAATGGTGGCTTTATCAAGAGAGTCCCTATCCACGGCCAGGAAC	1339
Db	361	GlyProAsnTyrGlnTrpValProTyrGlnGlyArgValProTyrProArgProGlyThr	380
QY	1340	TGTCCAGCAAAACATTTGGTGGTTTGCATCTACAAAGGACCTTCTGATGATGTATA	1399
Db	381	CysProSerLysThrPheGlyPheAspSerThrLysAspLeuProAspAspValIle	400
QY	1400	ACCTTTGCAAGAAGTCATCCAGCCATGACAAATCCAGTGTTCCTATGAACAATCGGCCA	1459
Db	401	ThrPheAlaArgSerHisProAlaMetTyrAsnProValPheProMetAsnAsnArgPro	420
QY	1460	ATAGTGATCAAAACCGATGTAAATTTATCAATTTACAAATTTGCTAGACCGAGTGGAT	1519
Db	421	IleValIleLysThrAspValAsnTyrGlnPheThrGlnIleValValAspArgValAsp	440
QY	1520	GCAGAGATGACAGTATGATGTATGTTATCCGACACAGATGTTGGACCGTCTTAAA	1579
Db	441	AlaGluAspGlyGlnTyrAspValMetPheIleGlyThrAspValGlyThrValLeuLys	460
QY	1580	GTAGTTTCAATTCCTAAGGAGACTTGGTATGATTAGAGAGGTTCTGCTCGAAGAAATG	1639
Db	461	ValValSerIleProLysGluThrTrpTyrAspLeuGluValLeuLeuGluMet	480
QY	1640	ACAGTTTTTCGGAAACCGACTGCTATTTTACGAAATGGAGCTTCCACTAAGCCACCAAA	1699
Db	481	ThrValPheArgGluProThrAlaIleSerAlaMetGluLeuSerThrLysGlnGln	500
QY	1700	CTATATATTGGTTCAACGGCTGGGGTGGCCAGTCCCTTACACCGGTGTGATATTAC	1759
Db	501	LeuTyrIleGlySerThrAlaGlyValAlaGlnLeuProLeuHisArgCysAspIleTyr	520
QY	1760	GGGAAAGCGTGTGCTGAGTGTGCTCGCCGAGACCTTACTTGTGCTGGATGGTTCT	1819
Db	521	GlyLysAlaCysAlaGluCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlySer	540
QY	1820	GCATGTTCTCGCTATTTTCCCACTGCAAGAGAGACCAAGACGACCAAGATATAAGAAAT	1879
Db	541	AlaCysSerArgTyrPheProThrAlaLysArgThrArgArgGlnAspIleArgAsn	560
QY	1880	GGAGACCCACTGACTCTGTTTACAGCTTACACCATGATAATCACCATGGCCACAGCCCT	1939
Db	561	GlyAspProLeuThrHisCysSerAspLeuHisHisAspAsnHisGlyHisSerPro	580
QY	1940	GAAGAGAGATCATCTATGGTGTAGAGATAGTACACATTTTTCGAATGTCAGTCCGAG	1999
Db	581	GluGluArgGlyIleTyrGlyValGluAsnSerSerThrPheLeuGluCysSerProLys	600
QY	2000	TCCGACAGAGCGCTGCTTATTGGCAATTTCCAGACGCCAAATGAAGACGAAAGAAAGAG	2059
Db	601	SerGlnArgAlaLeuValTyrTrpGlnPheGlnArgArgAsnGluGluArgLysGluGlu	620
QY	2060	ATCAGAGTGGATCATATCATCAGGACAGATCAGGCCCTTCTGCTACGTAGTCTACAA	2119
Db	621	IleArgValAspAspHisIleIleArgThrAspGlnGlyLeuLeuLeuArgSerLeuGln	640

QY 2120 CAGAGGATTGAGCAATTAACCTCTGCGCATGGTGAACATGGGTTTACACAACTCTT 2179
Db 641 GlnLysAspSerGlyAsnTyrLeuCySHisAlaValGluHisGlyPheIleGlnThrLeu 660
QY 2180 CTTAAGGTAACTTGGAGTCAATGACACAGAGCATTTGGAAGAACTTCTTCATAAAGAT 2239
Db 661 LeuLysValThrLeuGluValIleAspThrGluHisLeuGluGluLeuLeuHisLysAsp 680
QY 2240 GATGATGAGATGGCTCTAAGACCAAGAAATGTCCAAATAGCATGACACCTAGCCAGAAG 2299
Db 681 AspAspGlyAspGlySerLysThrLysGluMetSerAsnSerMetThrProSerGlnLys 700
QY 2300 GTCTGTACAGAGACTTCATCAGCTCATCAACCAACCCCAATCTCAACAGATGGATGAG 2359
Db 701 ValTrpTyrArgAspPheMetGlnLeuIleAsnHisProAsnLeuAsnThrMetAspGlu 720
QY 2360 TTCTGTGAACAAGTTTGGAAAGGAGCGGAAACACAGCTGGCAAGGCGCAGGACATACC 2419
Db 721 PheCysGluGlnValTrpLysArgAspArgLysGlnArgGlnArgProGlyHisThr 740
QY 2420 CCAGGGAACAGTAACAATGAAGCACTTACAAGAAATAGAAGGTGAAGACAGGAGG 2479
Db 741 ProGlyAsnSerAsnLysTrpLysHisLeuGlnGluAsnLysLysGlyArgAsnArgArg 760
QY 2480 ACCACGAAATTTGAGAGCGCACCCAGGAGTCTC 2512
Db 761 ThrHisGluPheGluArgAlaProArgSerVal 771

RESULT 2
US-08-835-268-54
; Sequence 54: Application US/08835268
; Patent No. 5807826
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey S.
; APPLICANT: Kolodkin, Alex L.
; APPLICANT: Matthes, David
; APPLICANT: Bentley, David R.
; APPLICANT: O'Connor, Timothy
; TITLE OF INVENTION: The Semaphorin Gene Family
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 Bush Street, Suite 3200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/835,268
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/121,713
; FILING DATE: 13-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B94-002-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; TELEX:
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 771 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-835-268-54
Alignment Scores:
Pred. No.: 0 Length: 771
Score: 771.00 Matches: 771
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 86.15% Indels: 0
DB: 1 Gaps: 0
US-09-774-490-1 (1-2709) x US-08-835-268-54 (1-771)
QY 200 ATGGCGTGTAACTAGGATTCTCTCTTTCTGGGAGTATTACTTACACAGAGCA 259
Db 1 MetGlyTrpLeuThrArgIleValCysLeuPheTrpGlyValLeuLeuThrAlaArgAla 20
QY 260 AACTATCACAATGGGAAGAACAAATGTGCCAAGCGTGAATATCTCACAAGAAATGTGT 319
Db 21 AsnTyrGlnAsnGlyLysAsnValProArgLeuLysLeuSerTyrLysGluMetLeu 40
QY 320 GAATCCACAATGTGATCACTTTCAATGGCTTGGCCAAACAGCTCCAGTTATCATCCTTC 379
Db 41 GluSerAsnValIleThrPheAsnGlyLeuAlaAsnSerSerSerTyrHisThrPhe 60
QY 380 CTTTGTGATGAGGAGGAGTAGGTGTATGTGGAGCAAGAGATCACATATTTTCATTC 439
Db 61 LeuLeuAspGluArgSerArgLeuTyrValGlyAlaLysAspHisIlePheSerPhe 80
QY 440 GACCTGTTAATATCAAGGATTTTCAAAAGATTTGTGTGCCAGTATCTTTACACCAAGA 499
Db 81 AspLeuValAsnIleLysAspPheGlnLysIleValTrpProValSerTyrThrArgArg 100
QY 500 GATGAATGCAAGTGGCTCGAAAAGACATCTCGAAGATGTCTAAATTTTCATCAAGTA 559
Db 101 AspGluCysLysTrpAlaGlyLysAspIleLeuLysGluCysAlaAsnPheIleLysVal 120
QY 560 CTTAAGGCATATAATCAGACTCACTTGTACGGCTGTGGAACGGGGCTTTTCATCCAAT 619
Db 121 LeuLysAlaTyrAsnGlnThrHisLeuTyrAlaCysGlyThrGlyAlaPheHisProIle 140
QY 620 TGCACCTACATTGCAATTCGATCATCTCTGAGGACATATTTTAAAGCTGGAGAACTCA 679
Db 141 CysThrTyrIleGluIleGlyHisHisProGluAspAsnIlePheLysLeuGluAsnSer 160
QY 680 CATTTTGAACGGCGTGGAGAGTCCATATGACCTTAAGCTGCTGACAGATCCCTT 739
Db 161 HisPheGluAsnGlyArgGlyLysSerProTyrAspProLysLeuLeuThrAlaSerLeu 180
QY 740 TTAATAGATGGAGATTAATATCTCTGAACTGCACTGATTTTATGGGCGAGACTTTGCT 799
Db 181 LeuIleAspGlyGluLeuTyrSerGlyThrAlaAlaAspPheMetGlyArgAspPheAla 200
QY 800 ATCTTCCGAACCTTGGGACACCCCAATCAGACAGACAGCATGATTCAGGTGG 859
Db 201 IlePheArgThrLeuGlyHisHisProIleArgThrGluGlnHisAspSerArgTrp 220
QY 860 CTCAATGATCCAAAGTTCAATTAAGTGCCACCTCATCTCAGAGAGTGACAAATCCTGAAGAT 919
Db 221 LeuAsnAspProLysPheIleSerAlaHisLeuIleSerGluSerAspAsnProGluAsp 240
QY 920 GACAAAGTATATCTTTTCTCGTGAAATGCAATAGATGGAGACACTCTGCGAAAGCT 979
Db 241 AspLysValTyrPhePheArgGluAsnAlaIleAspGlyGluHisSerGlyLysAla 260
QY 980 ACTCAGCTAGATAGTGCAGATATGCAAGATGACTTTGGAGGGCAGACAGATCTGGTG 1039
Db 261 ThrHisAlaArgIleGlyGlnIleCysLysAsnAspPheGlyHisArgSerLeuVal 280
QY 1040 AATAAATGGACAACTTCTCAAAGCTCGTCTCATTTGCTAGTGCAGGTCAAATGCG 1099
Db 281 AsnLysTrpThrThrPheLeuLysAlaArgLeuIleCysSerValProGlyProAsnGly 300
QY 1100 ATTGACACTCATTTTGTATGAACTGCAGGAGTGTATTCCTTAATGAACCTTAAAGATCCTAAA 1159

Db 301 IleAspThrHisPheAspGluLeuGlnAspValPheLeuMetAsnPhelYsAspProLys 320
Qy 1160 AATCCAGTTGATATGAGTGTTCAGACTCCAGTAACATTTCAAGGGATCAGCCGNG 1219
Db 321 AsnProValValTyGlyValPheThrThrSerSerAsnIlePhelYsGlySerAlaVal 340
Qy 1220 TGTATGATATGACATGATGTGAGAAAGGTTGCTTCTGTCATATGCCACAGGGAT 1279
Db 341 CysMetTySerMetSerAspValArgValPheLeuGlyProTyAlaHisArgAsp 360
Qy 1280 GGACCCAACTATCAATGGGTGCTTATCAAGGAAGTCCCTATCCACGCCCAGAACT 1339
Db 361 GlyProAsnTyGlnTrpValProTyGlnGlyArgValProTyProArgProGlyThr 380
Qy 1340 TGTCACGCAAAACATTTGGTGGTTTGACTCTACAAAGACCTTCTGATGATGTATA 1399
Db 381 CysProSerTyThrPheGlyGlyPheAspSerThrIlyshsAspLeuProAspValIle 400
Qy 1400 ACCTTTCAGAGACTATCCAGCCATCAATCCAGTGTTCCTATGAACAATCCGCCA 1459
Db 401 ThrPheAlaArgSerHisProAlaMetTyAsnProValPheProMetAsnAsnArgPro 420
Qy 1460 ATAGTGATCAAAACGGATGAATATCAATTTACACAAATTCGTPAGACCGAGTGGAT 1519
Db 421 IleValIleYsThrAspValAsnTyGlnPheThrGlnIleValValAspArgValAsp 440
Qy 1520 CCAGAAGATGACAGTATGATGTTATGTTATCGGAACAGATGTGGACCGTCTTAA 1579
Db 441 AlaGluAspGlyGlnTyAspValMetPheIleGlyThrAspValGlyThrValLeuLys 460
Qy 1580 GTAGTTCAATCTCCTAAGGAGACTGTGTATGATTAAGAGGTTCTGCTGGAGAAATG 1639
Db 461 ValValSerIleProLysGluThrTrpTyAspLeuGluValLeuLeuGluMet 480
Qy 1640 ACAGTTTTCGGGAACCGACTGCTATTTTCAGCAATGAGCTTTCACATAGACGCAACA 1699
Db 481 ThrValPheArgGluProThrAlaIleSerAlaMetGluLeuSerThrLysGlnGln 500
Qy 1700 CTATATATGTTCAACGGTGGGTTGCCAGTCCCTTTACACCGTGTGATATTAC 1759
Db 501 LeuTyIleGlySerThrAlaGlyValAlaGlnLeuProLeuHisArgCysAspIleTy 520
Qy 1760 GGGAAAGCGTGTGAGTGTGTGCTCCCGAGACCTTACTGTGTGGATGGTCT 1819
Db 521 GlyLysAlaCysAlaGluCysLeuAlaArgAspProTyCysAlaTrpAspGlySer 540
Qy 1820 GCATGTTCTCGCTATTTTCCCACTGCCAAGAGACGCAAGACCAAGATATAAGAAAT 1879
Db 541 AlaCysSerArgTyPheProThrAlaLysArgArgThrArgArgGlnAspIleArgAsn 560
Qy 1880 CGAGACCCACTGACTCATCTGTCAGACTTACACCATGATATCATCCATGGCCACAGCCT 1939
Db 561 GlyAspProLeuThrHisCysSerAspLeuHisAspAsnHisHisGlyHisSerPro 580
Qy 1940 GAAGAGAAATCATCTATGTTGTAGATAATAGTACACATTTTGGATCGAGTCCGAAG 1999
Db 581 GluGluArgIleIleTyGlyValGluAsnSerSerThrPheLeuGluCysSerProLys 600
Qy 2000 TCGCAGAGCGCTGCTGCTTATTTGCAATTCAGAGGCGAATGAAGCGCAAGAGAGAG 2059
Db 601 SerGlnArgAlaLeuValTyTrpGlnPheGlnArgArgAsnGluGluArgLysGluGlu 620
Qy 2060 ATCAGATGGATGATCATATCATCAGGACAGATCAAGGCCCTTCTGCTACGTAGTCTCAA 2119
Db 621 IleArgValAspAspHisIleIleArgThrAspGlnGlyLeuLeuLeuLeuSerLeuGln 640
Qy 2120 CAGAAGGATTCAGGAATTTACTCTGTCATCGGTGGAAACATGGGTTCATACAACTCTT 2179
Db 641 GlnLysAspSerGlyAsnTyLeuCysHisAlaValGluHisGlyPheIleGlnThrLeu 660
Qy 2180 CTTAAGGTAACCTCGAAGTCAATTCACACAGAGACTTTGGAAGAACTTCTTCATAAAGAT 2239

Db 661 LeuLysValThrLeuGluValIleAspThrGluHisLeuGluGluLeuLeuHisLysAsp 680
Qy 2240 GATGATGGAGATGGCTCTTAAGACCAAAAGAAATGTCCAAATAGCATGACACCTAGCCAGAAG 2299
Db 681 AspAspGlyAspGlySerLysThrLysGluMetSerAsnSerMetThrProSerGlnLys 700
Qy 2300 GTCTGTCACAGAGACTTCATGACGCTCATCAACCAACCCCAATCTCAACACAGATGGATGAG 2359
Db 701 ValTrpTyArgAspPheMetGlnLeuIleAsnHisProAsnLeuAsnThrMetAspGlu 720
Qy 2360 TTCTGTGAACCAAGTTTGAAAGGACCGCAAAACACAGCTCGGCAAGGCCAGGACATACC 2419
Db 721 PheCysGluGlnValTrpLysArgAspArgLysGlnArgGlnArgProGlyHisThr 740
Qy 2420 CCAGGAAACAGTATCAAAATGGAAGCACTTACAAAGAAATGAAGAGGTAGAAACAGGAGG 2479
Db 741 ProGlyAsnSerAsnLysTrpLysHisLeuGlnGluAsnLysLysGlyArgAsnArg 760
Qy 2480 ACCCAGCAATTTGAGAGGCGCACCCAGGAGTGTC 2512
Db 761 ThrHisGluPheGluArgAlaProArgSerVal 771
RESULT 3
US-09-060-692-54
; Sequence 54, Application US/09060692
; Patent No. 5935865
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey S.
; APPLICANT: Kolodkin, Alex L.
; APPLICANT: Matthes, David
; APPLICANT: Bentley, David R.
; APPLICANT: O'Connor, Timothy
; TITLE OF INVENTION: The Semaphorin Gene Family
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSES: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 Bush Street, Suite 3200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/060,692
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/121,713
; FILING DATE: 13-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B94-002-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)343-4341
; TELEFAX: (415) 343-4342
; TELEX:
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 771 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-060-692-54
Alignment Scores:
Pred. No.: 0
Score: 771.00
Percent Similarity: 100.00%
Length: 771
Matches: 771
Conservative: 0

Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	86.15%	Indels:	0
DB:	2	Gaps:	0
US-09-774-490-1 (1-2709) x US-09-060-692-54 (1-771)			
QY	200	ATGGGCTGTTAACTAGGATTCGTGCTTTCTGGGAGATTACTTACAGCAAGACA	259
DB	1	MetGlyTrpLeuThrArgIleValCysLeuPheTrpGlyValLeuLeuThrAlaArgAla	20
QY	260	AACATCAAGATGGGAAGAACAAATGTGCCAGGTGAATATCTCAAGAAATGTG	319
DB	21	AsnTyrGlnAsnGlyLysAsnValProArgLeuLysLeuSerTyrLysGluMetLeu	40
QY	320	GAATCCAAAGTGCATCTTCAATGCTGGCCACAGCTCCAGTATCATACCTTC	379
DB	41	GluSerAsnAsnValIleThrPheAsnGlyLeuAlaAsnSerSerTyrHisThrPhe	60
QY	380	CTTTGGATGAGGACGGAGTAGGCTGTATGTTGGAGCAAGGATCACATATTTCA	439
DB	61	LeuLeuAspGluGluArgSerArgLeuTyrValGlyAlaLysAspHisPheSerPhe	80
QY	440	GACCTGGTATATCAAGATTTTCAAGATTTGTGGCCAGTATCTTACACAGAGA	499
DB	81	AspLeuValAsnIleLysAspPheGlnLysIleValTrpProValSerTyrThrArg	100
QY	500	GATGAATGCAAGTGGCTGGAAAGACATCTCGAAAGATGTCTAAATTCATCAAG	559
DB	101	AspGluCysLysTrpAlaGlyLysAspIleLeuLysGluCysAlaAsnPheIleLys	120
QY	560	CTTAAGGCATATAATCAGACTCACTGTGACGCTGTGGAACGGGGCTTTTCATC	619
DB	121	LeuLysAlaTyrAsnGlnThrHisLeuTyrAlaCysGlyThrGlyAlaPheHisP	140
QY	620	TGCACCTACATTAAGATGGACATCATCTGAGGACAATATTTTAAAGCTGGAGA	679
DB	141	CysThrTyrIleLeuIleGlyHisHisProGluAspAsnIlePheLysLeuGlu	160
QY	680	CATTTTGAACCGCGTGGAGAGTCCATATGACCTCAAGCTCTGACAGCATCCCT	739
DB	161	HisPheGluAsnGlyArgGlyLysSerProTyrAspProLysLeuLeuThrAla	180
QY	740	TAAATAGATGGAGATTACTCTGGAATCGAGCTGATTTTATGGGGGAGACTTTC	799
DB	181	LeuIleAspGlyGluLeuTyrSerGlyThrAlaAlaAspPheMetGlyArgAsp	200
QY	800	ATCTTCCGAACCTTGGGCACCAACCAATCAGGACAGACGACATTCACAGGTGG	859
DB	201	IlePheArgThrLeuGlyHisHisHisProIleArgThrGluGlnHisAspSer	220
QY	860	CTCAATGATCCAAAGTTCATAGTCCCACTCATCTCAGAGAGTGACAACTCTGA	919
DB	221	LeuAsnAspProLysPheIleSerAlaHisLeuIleSerGluSerAspAsnPro	240
QY	920	GACAAAGTATCTTTTCTTCGTAAGATCAATAGATGAGAACACTCTGGAAAGCT	979
DB	241	AspLysValTyrPhePheArgGluAsnAlaIleAspGlyGluHisSerGlyLys	260
QY	980	ACTCAGCTAGATAGGTGAGATATCCAAAGATGACTTTGGAGGACACAGAGTCT	1039
DB	261	ThrHisAlaArgIleGlyGlnIleCysLysAsnAspPheGlyGlyHisArgSer	280
QY	1040	ATAATAGCACACATCTCTCAAGCTCGTGTGATTTCTCAGTCCAGGTCCTCAAT	1099
DB	281	AsnLysTrpThrPheLeuLysAlaArgLeuIleCysSerValProGlyProAsn	300
QY	1100	ATTGACACCTATTTGATGAATGCGAGGATGATTCCTTAATGAATTTAAAGATC	1159
DB	301	IleAspThrHisPheAspGluLeuGlnAspValPheLeuMetAsnPheLysAsp	320
QY	1160	ATCCAGTTGTATAGGAGTGTTCAGACTTCCAGTACATTTTCAAGGGATCAGCC	1219
DB	321	AsnProValValTyrGlyValPheThrThrSerSerAsnIlePheLysGlySer	1340

QY	1220	TGTATGTATAGCATGATGATGTGAGAGGGTGTCTCTGGTCCATATGCCACAGG	1279
DB	341	CysMetTyrSerMetSerAspValArgValPheLeuGlyProTyrAlaHisArgSp	360
QY	1280	GGACCCAACTATCAATGGGTGCCTTATCAAGGAAGAGTCCCTTATCCAGCCAG	1339
DB	361	GlyProAsnTyrGlnTrpValProTyrGlnGlyArgValProTyrProArgPro	380
QY	1340	TGTCACGCAAAACATTTGGTGGTTTGTACTCTACAAAGGACCTTCTGTATG	1399
DB	381	CysProSerLysThrPheGlyGlyPheAspSerThrLysAspLeuProAspVal	400
QY	1400	ACCTTTGCCAAAGATCATCCAGCCATGATCAATCCAGTGTTCCTATGAACAAT	1459
DB	401	ThrPheAlaArgSerHisProAlaMetTyrAsnProValPheProMetAsnAsn	420
QY	1460	ATAGTGATCAAAACGGATGTAATATCAATTTACAAATTTCTGTAGACCGAGT	1519
DB	421	IleValIleLysThrAspValAsnTyrGlnPheThrGlnIleValValAspArg	440
QY	1520	GCAGAGATGCAGATGATGTATGTTTATCGGAACAGATGTTGGACCGTCTTAA	1579
DB	441	AlaGluAspGlyGlnTyrAspValMetPheIleGlyThrAspValGlyThrVal	460
QY	1580	GTAAGTTTCAATCTTAAAGGAGACTTGTATGATTTAGAAAGAGTTCTGCTG	1639
DB	461	ValValSerIleProLysGluThrTyrTyrAspLeuGluGluValLeuLeuGlu	480
QY	1640	ACAGTTTTCGGAAACCGACTGCTATTTACAGCAATGGAGCTTTCCTAAGCAG	1699
DB	481	ThrValPheArgGluProThrAlaIleSerAlaMetGluLeuSerThrLysGln	500
QY	1700	CTATATATTGGTTCAACGGCTGGGGTTCGCCAGCTCCCTTTACACGGGTGAT	1759
DB	501	LeuTyrIleGlySerThrAlaGlyValAlaGlnLeuProLeuHisArgCysAsp	520
QY	1760	GGGAAACGCTGCTGAGTGTTGCTCGCCCGAGAGACCTTACTGCTGCTGGATG	1819
DB	521	GlyLysAlaCysAlaGluCysCysLeuAlaArgAspProTyrCysAlaTrpAsp	540
QY	1820	GCATGTTCTCGCTATTTCCACTGCAAGAGAGACGACAAAGACACAAAGATA	1879
DB	541	AlaCysSerArgTyrPheProThrAlaLysArgArgThrArgGlnAspIleArg	560
QY	1880	GGAGACCACTGACTCAGCTTTCAGACTTACACCATGATAATCACCATGCCAC	1939
DB	561	GlyAspProLeuThrHisCysSerAspLeuHisHisAspAsnHisGlyHisSer	580
QY	1940	GAAGAGAAATCATCTCTGCTGAGCAATAGTACACATTTTGGAAATGCACTCC	1999
DB	581	GluGluArgIleIleTyrGlyValGluAsnSerThrPheLeuGluCysSerPro	600
QY	2000	TCGCAGAGAGCGCTGTTCTTATTTGGCAATTCAGAGCGGCAATGAAGAGGAG	2059
DB	601	SerGlnArgAlaLeuValTyrTrpGlnPheGlnArgArgAsnGluGluArgLys	620
QY	2060	ATCAGAGTGATGATCATATCATCAGACAGATCAAGGCCTTCTGTACGTAGTAC	2119
DB	621	IleArgValAspAspHisIleIleArgThrAspGlnGlyLeuLeuLeuArgSer	640
QY	2120	CAGAAGGATTTCAGCAATTAACCTCTGCGATGCGGTGGAACATGGTTCATAC	2179
DB	641	GlnLysAspSerGlyAsnTyrLeuCysHisAlaValGluHisGlyPheIleGln	660
QY	2180	CTTAAGTAAACCTTGAAGTCAATTGACACAGACATTTGGAAGAACTTCTTCA	2239
DB	661	LeuLysValThrLeuGluValIleAspThrGluHisLeuGluGluLeuHisLys	680
QY	2240	GATCATGGAGATGGCTCTAGACCAAGAAATGTCCAAATAGCATGACACCTACC	2299
DB	681	AspAspGlyAspGlySerLysThrLysGluMetSerAsnSerMetThrProSer	700

QY 2300 GTCTGGTACAGAGACTTCATGCACTCATCAACACACCCCAATCTCAACACGATGGATGAG 2359
 Db 701 ValTrpYrArgAspPheMetGlnLeuIleAsnHisProAsnLeuAsnThrMetAspGlu 720
 QY 2360 TTCTGTGACAAAGTTCGAAAGGGACCGAAACACAGCTCGGCAAGGCCAGGACATACC 2419
 Db 721 PheCysGluGlnValTrpLysArgAspArgLysGlnArgGlnArgProGlyHisThr 740
 QY 2420 CCAGGGAACAGTAACAAATGGAACACTTCAAGAAATAAGAAAGGTAGAAACAGAGG 2479
 Db 741 ProGlyAsnSerAsnLysTrpLysHisLeuGlnGluAsnLysLysGlyArgAsnArgArg 760
 QY 2480 ACCACAGATTGAGAGGGACCCAGGAGTGC 2512
 Db 761 ThrHisGluPheGluArgAlaProArgSerVal 771

RESULT 4
 US-08-833-391-54
 ; Sequence 54, Application US/08833391
 ; GENERAL INFORMATION:
 ; APPLICANT: Goodman, Corey S.
 ; APPLICANT: Kolodkin, Alex L.
 ; APPLICANT: Matthes, David
 ; APPLICANT: Bentley, David R.
 ; APPLICANT: O'Connor, Timothy
 ; TITLE OF INVENTION: The Semaphorin Gene Family
 ; NUMBER OF SEQUENCES: 100
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
 ; STREET: 268 Bush Street, Suite 3200
 ; CITY: San Francisco
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94104
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/833,391
 ; FILING DATE:
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/121,713
 ; FILING DATE: 13-SEP-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Osman, Richard A.
 ; REGISTRATION NUMBER: 36,627
 ; REFERENCE/DOCKET NUMBER: B94-002-1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 343-4341
 ; TELEFAX: (415) 343-4342
 ; TELETYPE:
 ; INFORMATION FOR SEQ ID NO: 54:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 771 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-833-391-54
 Alignment Scores:
 Pred. No.: 0 Length: 771
 Score: 771.00 Matches: 771
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 86.15% Indels: 0
 DB: 3 Gaps:
 US-09-774-490-1 (1-2709) x US-08-833-391-54 (1-771)

QY 200 ATGGGCTGGTTAACTAGGATTGTCTGCTTTTCTGGGAGTATTACTTACAGCAAGACGA 259
 Db 1 MetGlyTrpLeuThrArgGileValCysLeuPheTrpGlyValLeuLeuThrAlaArgAla 20
 QY 260 AACTATCAAGATGGGAAGCAACAATCTGCCAAGGTGAAATATCTCAAGAAATCTTG 319
 Db 21 AsnTyrGlnAsnGlyLysAsnValProArgLeuLysLeuSerTyrLysGluMetLeu 40
 QY 320 GAATCCAAATATGATACATTTCAATGGCTTGGCCACACAGCTCCAGTTATCATACCTC 379
 Db 41 GluSerAsnAsnValIleThrPheAsnGlyLeuAlaAsnSerSerSerTyrHisThrPhe 60
 QY 380 CTTTGGATGAGGAACGAGTAGGTGTATCTTGGCAAGGATCATATTTTCAATTC 439
 Db 61 LeuLeuAspGluArgSerArgLeuTyrValGlyAlaLysAspHisIlePheSerPhe 80
 QY 440 GACCTGGTTAATATCAAGGATTTTCAAAAGATTGTGTGGCCACATCTTACACCAAGAGA 499
 Db 81 AspLeuValAsnIleLysAspPheGlnLysIleValTrpProValSerTyrThrArgArg 100
 QY 500 GATGAATGCACTGGCTGGAAAGACATCTCTGAAGAAATGTCTAATTTTCAATCAAGTA 559
 Db 101 AspGluCysLysTrpAlaGlyLysAspIleLeuLysGluCysAlaAsnPheIleLysVal 120
 QY 560 CTTAAGGCATATAATCAGACTCATTTGACGCTGTGGAACGGGGGCTTTTCATCCAAT 619
 Db 121 LeuLysAlaTyrAsnGlnThrHisLeuTyrAlaCysGlyThrGlyAlaPheHisProIle 140
 QY 620 TGCACCTACATTAATTTGGACATCATCTGAGGACATATTTTAACTCGGAGAACTCA 679
 Db 141 CysThrTyrIleGluIleGlyHisHisProGluAspAsnIlePheLysLeuGluAsnSer 160
 QY 680 CATTGTGAAAACGGCGCTGGGAAGAGTCCATATGACCTTAAGCTCTCAGACGATCCCT 739
 Db 161 HisPheGluAsnGlyArgGlyLysSerProTyrAspProLysLeuLeuThrAlaSerLeu 180
 QY 740 TTAATAGATGAGAAATTTACTCTGGAACCTGAGCTGATTTTATGGGCGAGACTTCT 799
 Db 181 LeuIleAspGlyGluLeuTyrSerGlyThrAlaAspPheMetGlyArgAspPheAla 200
 QY 800 ATCTTCCGAACCTCTTTGGGCAACCCACCACTCAGGACAGACGACATGATTCAGSTGG 859
 Db 201 IlePheArgThrLeuGlyHisHisProIleArgThrGluGlnHisAspSerArgTrp 220
 QY 860 CTCATATGATCCAAAGTTCATTTAGTCCCACTCATCTCAGAGAGTGACAATCTGAAAGT 919
 Db 221 LeuAsnAspProLysPheIleSerAlaHisLeuIleSerGluSerAspAsnProGluAsp 240
 QY 920 GACAAAGTATACCTTTTCTTCGTCGAAATGCAATAGATGGAGAACACTCTGGAAAAGCT 979
 Db 241 AspLysValTyrPhePhePheArgGluAsnAlaIleAspGlyGluHisSerGlyLysAla 260
 QY 980 ACTCAGCTAGAAATAGGTGAGATATGCAAGAAATGCTTTGGAGGGCACAGAGTCTGGTG 1039
 Db 261 ThrHisAlaArgIleGlyGlnIleCysLysAsnAspPheGlyHisArgSerLeuVal 280
 QY 1040 AATAAATGCAACACATTTCTCAAGCTCGTCTGATTTGCTCAGTCCAGGTCCCAATGGC 1099
 Db 281 AsnLysTrpThrPheLeuLysAlaArgLeuIleCysSerValProGlyProAsnGly 300
 QY 1100 ATTGACACTCATTTTGTATGAACTGAGGATGATTTCTTAATGAATTTAAAGATCCTAAA 1159
 Db 301 IleAspThrHisPheAspGluLeuGlnAspValPheLeuMetAsnPheLysAspProLys 320
 QY 1160 ATCCAGTTGTATATGAGTGTTCAGCTTTTACGATTTCCAGTAACTTTTCAAGGGATCACCCGTG 1219
 Db 321 AsnProValValTyrGlyValPheThrThrSerSerAsnIlePheLysGlySerAlaVal 340
 QY 1220 TGTATGTATAGATGATGATGTGAGAGGGTGTTCCTTGTGTCCATATGCCACAGGAT 1279
 Db 341 CysMetTyrSerMetSerAspValArgValPheLeuGlyProTyrAlaHisArgAsp 360
 QY 1280 GGACCAACTATCAATGGGTGCTTATCAAGAAAGTCCCTATCCACGGCCAGGAAC 1339

Db 361 GlyProAsnTyrGlnTrpValProTyrGlnGlyArgValProTyrProArgProGlyThr 380
QY 1340 TGTCACCAACAAATTTGGTGGTTTGGTACCTCAACAAAGGACCTTCTGTGATGATGTTATA 1399
Db 381 CysProSerLysThrPheGlyGlyPheAspSerThrLysAspLeuProAspAspValIle 400
QY 1400 ACCTTTGCAGAGTCATCCAGCATGATACAAATCCAGTGTTTCTCTATGAACAATCGCCCA 1459
Db 401 ThrPheAlaArgSerHisProAlaMetTyrAsnProValPheProMetAsnAsnArgPro 420
QY 1460 ATAGTGATCAAAACCGATGTAATTTATCAATTTACAAATTTGCTAGACCGAGTGGAT 1519
Db 421 IleValIleLysThrAspValAsnTyrGlnPheThrGlnIleValValAspArgValAsp 440
QY 1520 GCAGAAAGTCACAGTATGATGTTATGTTATCGGAACAGATGTGGACCGTTCTTAA 1579
Db 441 AlaGluAspGlyGlnTyrAspValMetPheIleGlyThrAspValGlyThrValLeuLys 460
QY 1580 GTAGTTTCAATTCCTAAGGACCTGGTATGATTTAGAGAGGTTCTGCTGGAAGAATG 1639
Db 461 ValValSerIleProLysGluThrTrpTyrAspLeuGluGluValLeuLeuGluGluMet 480
QY 1640 ACAGTTTTCGGGAACCGATGCTATTTTCAGCAATGGAGCTTTCCTACTAAGCAGCAACA 1699
Db 481 ThrValPheArgGluProThrAlaIleSerAlaMetGluLeuSerThrLysGlnGln 500
QY 1700 CTATATATGTTTCAACGGCTGGGGTTCGCCAGCTCCCTTTACACCGGTGTGATTTAC 1759
Db 501 LeuTyrIleGlySerThrAlaGlyValAlaGlnLeuProLeuHisArgCysAspIleTyr 520
QY 1760 GGGAAAGCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1819
Db 521 GlyLysAlaCysAlaGluCysLeuAlaArgAspProTyrCysAlaTrpAspGlySer 540
QY 1820 GCATGTTCTCGCTATTTTCCACTGCAAGAGAGCAGCAACAGCAAGATATAGAAAT 1879
Db 541 AlaCysSerArgTyrPheProThrAlaLysArgThrArgGlnAspIleArgAsn 560
QY 1880 GGAGACCACTGACTCCTGTTTCAGCTTACACCATGATATATCACCATGGCCAGAGCCT 1939
Db 561 GlyAspProLeuThrHisCysSerAspLeuHisAspAsnHisGlyHisSerPro 580
QY 1940 GAAGAGAGATCATCTATGTTGATAGAAATAGTACACATTTTGGAAATGCAAGTCCGAAG 1999
Db 581 GluGluArgIleIleTyrGlyValGluAsnSerSerThrPheLeuGluCysSerProLys 600
QY 2000 TCGCAGAGAGCGCTGCTATTTGGCAATTCAGAGCGCAATAGAGCGCAATAGAGCGCAAG 2059
Db 601 SerGlnArgAlaLeuValTyrTrpGlnPheGlnArgArgAsnGluArgLysGluGlu 620
QY 2060 ATCAGAGTGGATGATCATATCATCAGGACAGATCAAGGCCTTCTGCTACGTAGTCTACAA 2119
Db 621 IleArgValAspAspHisIleIleArgThrAspGlnGlyLeuLeuLeuArgSerLeuGln 640
QY 2120 CAGAGAGATTCAGGCAATTTACCTGTCATCGCTGGTGGCAATGGGTTTCATCAACACTCTT 2179
Db 641 GlnLysAspSerGlyAsnTyrLeuCysHisAlaValGluHisGlyPheIleGlnThrLeu 660
QY 2180 CTTRAGGTAACTCGGAGTCAATTCAGCAGAGCAATTTGGAAGACTTCTTCATAAAGAT 2239
Db 661 LeuLysValThrLeuGluValIleAspThrGluHisLeuGluGluLeuLeuHisLysAsp 680
QY 2240 GATGATGGAGATGGCTCTAAGACCAAGAAATGTCCTCAATAGCATGACACCTAGCCAGAG 2299
Db 681 AspAspGlyAspGlySerLysThrLysGluMetSerAsnSerMetThrProSerGlnLys 700
QY 2300 GTCTGGTACAGAGCTTCATGAGCTCATCAACACCCCACTCTCAACAGCATGATGATAG 2359
Db 701 ValTrpTyrArgAspPheMetGlnLeuIleAsnHisProAsnLeuAsnThrMetAspGlu 720
QY 2360 TTCTGTGACAAAGTTTGGAAAAGGACCGGAAACAACTCGGCAAGGCCAGGACATACC 2419

Db 721 PheCysGluGlnValTrpLysArgAspArgLysGlnArgGlnArgProGlyHisThr 740
QY 2420 CCAGGGAACAGTAACAATGGAAGCAGCTTACAGAAATAAGAAAGGTAGAAACAGGAGG 2479
Db 741 ProGlyAsnSerAsnLysTrpLysHisLeuGlnGluAsnLysGlyArgAsnArgArg 760
QY 2480 ACCCAGCAATTTCCAGAGGCGCACCCAGGAGCTGTC 2512
Db 761 ThrHisGluPheGluArgAlaProArgSerVal 771
RESULT 5
US-09-060-610-54
: Sequence 54, Application US/09060610
: Patent No. 6344544
: GENERAL INFORMATION:
: APPLICANT: Goodman, Corey S.
: APPLICANT: Kolodkin, Alex L.
: APPLICANT: Matthes, David
: APPLICANT: Bentley, David R.
: APPLICANT: O'Connor, Timothy
: TITLE OF INVENTION: The Semaphorin Gene Family
: NUMBER OF SEQUENCES: 100
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
: STREET: 268 Bush Street, Suite 3200
: CITY: San Francisco
: STATE: CA
: COUNTRY: USA
: ZIP: 94104
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/060,610
: FILING DATE:
: CLASSIFICATION:
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: 08/835,268
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Osman, Richard A.
: REGISTRATION NUMBER: 36,627
: REFERENCE/DOCKET NUMBER: B94-002-1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 343-4341
: TELEFAX: (415) 343-4342
: TELEX:
: INFORMATION FOR SEQ ID NO: 54:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 771 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-09-060-610-54
Alignment Scores:
Pred. No.: 0 Length: 771
Score: 771.00 Matches: 771
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 86.15% Indels: 0
DB: 4 Gaps: 0
US-09-774-490-1 (1-2709) x US-09-060-610-54 (1-771)
QY 200 ATGGCTGGTAACTAGGATGCTCTCTTTCTGGGAGTATTACTTACAGCAAGCA 259
Db 1 MetGlyTrpLeuThrArgIleValCysLeuPheTrpGlyValLeuLeuThrAlaArgAla 20
QY 260 AACTATCAGAAATGGGAGAACAAATGTGCCAAGCTGAAATTAATCTACAGAAATGTTG 319

Db 21 AsnTyrGlnAsnGlyLysAsnAsnValProArgLeuLysLeuSerTyrLysGluMetLeu 40
Qy 320 GAATCCAAACATGTGATCACTTTCAATGGCTGGCCAAACAGCTCCAGTTATCATCTTC 379
Db 41 GluSerAsnAsnValIleThrPheAsnGlyLeuAlaAsnSerSerTyrHisThrPhe 60
Qy 380 CTTTGGATGAGGAACGAGTAGGCTGTATGTTGGACAAAGGATCACATATTTTCATTC 439
Db 61 LeuLeuAspGluGluArgSerArgLeuTyrValGlyAlaLysAspHisIlePheSerPhe 80
Qy 440 GACCTGGTTAATCAAGGATTTTCAAAAGATTCTGTGGCCAGTATCTTACACCAAGA 499
Db 81 AspLeuValAsnIleLysAspPheGlnLysIleValTrpProValSerTyrThrArgArg 100
Qy 500 GATGAATCCAGTGGCTGGAAAGACATCTGTGAAGAATGCTGTAAATTTTCATCAAGGTÀ 559
Db 101 AspGluCysLysTrpAlaGlyLysAspIleLeuLysGluCysAlaAsnPheIleLysVal 120
Qy 560 CTTAAGGCATATAATCAGACTCACTTGTAGCCCTGTGGAACGGGGCTTTTCATCCAATT 619
Db 121 LeuLysAlaTyrAsnGlnThrHisLeuTyrAlaCysGlyThrGlyAlaPheHisProIle 140
Qy 620 TGCACCTACATGAAATTGGACATCCTCGAGACAAATATTTTAAGCTGGAGAACTCA 679
Db 141 CysThrTyrIleGluIleGlyHisHisProGluAspAsnIlePheLysLeuGluAsnSer 160
Qy 680 CATTTTGAACCGCGTGGGAAGAGTCCATATCACCTTAAGCTGTGACAGCATCCCTT 739
Db 161 HisPheGluAsnGlyA-glyLysSerProTyrAspProLysLeuLeuThrAlaSerLeu 180
Qy 740 TTAATAGATGAGAAATTATCTCTGGAACTGCACTGATTTTATGGGGCGAGACTTTGCT 799
Db 181 LeuIleAspGlyGluLeuTyrSerGlyThrAlaAlaAspPheMetGlyA-gaspPheAla 200
Qy 800 ATCTTCCAACTCTGGCCACACCCATCATAGAGACAGACAGCATGATTCAGGTGG 859
Db 201 IlePheArgThrLeuGlyHisHisProIleArgThrGluGlnHisAspSerArgTrp 220
Qy 860 CTCAATGATCAAAAGTTCAATAGTGGCCACCTCATCTCAGAGAGTGCATATCTCGAAGAT 919
Db 221 LeuAsnAspProLysPheIleSerAlaHisLeuIleSerGluSerAspAsnProGluAsp 240
Qy 920 GACAAAGTATCTTTTTCCTGGTAAATGCATAGATGAGACACTCTGGAAAGCT 979
Db 241 AspLysValTyrPhePhePheArgGluAsnAlaIleAspGlyGlyHisSerGlyLysAla 260
Qy 980 ACTCAGCTAGATAGTGCATATGCAAGAAATGACATTTGGAGGCGACAGAAGTCTGGTG 1039
Db 261 ThrHisAlaA-glyIleGlyGlnIleCysLysAsnAspPheGlyGlyHisArgSerLeuVal 280
Qy 1040 AATAAATCGAACAACTTCTCAAGCTCGTGTGATTTGCTCAGTGCAGGTCCAAATGGC 1099
Db 281 AsnLysTrpThrPheLeuLysAlaArgLeuIleCysSerValProGlyProAsnGly 300
Qy 1100 ATTGACACTCAATTTTGTGAATCGAGGATGTATTTCTTAATGAATTTAAAGATCTTAAA 1159
Db 301 IleAspThrHisPheAspGluGlnAspValPheLeuMetAsnPheLysAspProLys 320
Qy 1160 AATCAGCTGTATATGAGTGTTCACGACTTCCAGTAACTATTTCAAGGGATCAGCCGTG 1219
Db 321 AsnProValValTyrGlyValPheThrThrSerSerAsnIlePheLysGlySerAlaVal 340
Qy 1220 TGTATGTATACATGAGTGTGAGAGGGTGTCTTGGTCCATATGCCACAGGGAT 1279
Db 341 CysMetTyrSerMetSerAspValArgArgValPheLeuGlyProTyrAlaHisArgAsp 360
Qy 1280 GGACCCCAACTATCAATGGGTGCCCTTATCAAGGAAGAGTCCCTTATCCACGCCAGGAAC 1339
Db 361 GlyProAsnTyrGlnTrpValProTyrGlnGlyArgValProTyrProArgProGlyThr 380
Qy 1340 TGTCACGACAAACATTTGGTGGTTTTCACCTACAAAGGACCTTCTGTATGATGTTATA 1399
Db 381 CysProSerLysThrPheGlyGlyPheAspSerThrLysAspLeuProAspAspValIle 400

Qy 1400 ACCTTTGCAAGAAGTCATCCAGCCATGTACAATCCAGTGTTCCTATGAACAATCGCCCA 1459
Db 401 ThrPheAlaArgSerHisProAlaMetTyrAsnProValPheProMetAsnAsnArgPro 420
Qy 1460 ATAGTGATCAAAACGGATGTAAATTTATCAATTTACAAAATTCGTAGACCGAGTGAT 1519
Db 421 IleValIleLysThrAspValAsnTyrGlnPheThrGlnIleValValAspArgValAsp 440
Qy 1520 GCAGAGATGCACAGTATGATGTTATTCGGAACAGATGTTGGACCGTTCCTTAAA 1579
Db 441 AlaGluAspGlyGlnTyrAspValMetPheIleGlyThrAspValGlyThrValLeuLys 460
Qy 1580 GTAGTTTCAATTCCTAAGGAGACTTTGGTATGATGATTAGAAAGGTTCTGCTGGAATAATG 1639
Db 461 ValValSerIleProLysGluThrTrpTyrAspLeuGluValLeuLeuGluMet 480
Qy 1640 ACAGTTTTTGGGAACCGACTGCTATTTACAGAAATGGAGCTTCCACTAAGCAGCAAA 1699
Db 481 ThrValPheA-gluProThrAlaIleSerAlaMetGluLeuSerThrLysGlnGlnGln 500
Qy 1700 CTATATATTGGTTCAACGGCTGGGGTTCGCCAGCTCCCTTTACACCGGTGTGATATTAC 1759
Db 501 LeuTyrIleGlySerThrAlaGlyValAlaGlnLeuProLeuHisArgCysAspIleTyr 520
Qy 1760 GGGAAAGCGTGTGCTGAGTGTGCTCCCGAGACCTTACTGTGCTTGGGATGGTTCT 1819
Db 521 GlyLysAlaCysAlaGluCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlySer 540
Qy 1820 GCATCTTCTCCGTATTTTCCCACTGCAAGAGACGCAACAGACAGATATAGAAT 1879
Db 541 AlaCysSerArgTyrPheProThrAlaLysArgThrArgGlnAspIleArgAsn 560
Qy 1880 GGAGACCCACTGACTCACTGTTCAGACTTACACCATGATAATCACCATGGCCACAGCCCT 1939
Db 561 GlyAspProLeuThrHisCysSerAspLeuHisAspAsnHisGlyHisSerPro 580
Qy 1940 GAAGAGAAATCATCTATGTGTAGAGATAGTACCACATTTTGGATGTCAGTCCGAAG 1999
Db 581 GluGluA-glyIleTyrGlyValGluAsnSerThrPheLeuGluCysSerProLys 600
Qy 2000 TCCGACAGAGCGCTCGTCTATTGGCAATTCAGAGCGGAAATGAAGAGCGAAAACAAGAG 2059
Db 601 SerGlnArgAlaLeuValTyrTrpGlnPheGlnArgA-gAsnGluGluArgLysGluGlu 620
Qy 2060 ATCAGAGTGATGATCATATCATCAGGACAGATCAGGCCCTTCTGTACGTAGTCTACAA 2119
Db 621 IleArgValAspAspHisIleIleArgThrAspGlnGlyLeuLeuLeuAspSerLeuGln 640
Qy 2120 CAGAAAGATTCAAGCAATTCCTCTGCCATCGGTGGAAACATGGTTTCATCAAACTCTT 2179
Db 641 GlnLysAspSerGlyAsnTyrLeuCysHisAlaValGluHisGlyPheIleGlnThrLeu 660
Qy 2180 CTTAAGGTAAACCTCGAAGTCAATTCACAGAGCATTTGGAGAACTTCTTCATAAAGAT 2239
Db 661 LeuLysValThrLeuGluValIleAspThrGluHisLeuGluGluLeuLeuHisLysAsp 680
Qy 2240 GATGATGGAGTGGCTTAAGACCAAGAAATGTCCAATAGCATCAGACCTAGCCAGAGAG 2299
Db 681 AspAspGlyAspGlySerLysThrLysGluMetSerAsnSerMetThrProSerGlnLys 700
Qy 2300 GTCTGGTACAGAGACTTTCAGCTCATCAACCAACCCCAATCTCAACACCATGATGATG 2359
Db 701 ValTrpTyrArgAspPheMetGlnLeuIleAsnHisProAsnLeuAsnThrMetAspGlu 720
Qy 2360 TTCTGTGAACAATTTGGAAGGACCGAAACACCTCGCAAGAGCCAGGACATACC 2419
Db 721 PheCysGluGlnValTrpLysArgAspArgLysGlnArgA-gGlnArgProGlyHisThr 740
Qy 2420 CCAGGGAACAGTAACAAATGGAAGCACTTACAAGAAAAATAAGAAAGGTAGAAACAGGAGG 2479
Db 741 ProGlyAsnSerAsnLysTrpLysHisLeuGlnGluAsnLysLysGlyArgAsnArgArg 760

QY 2480 ACCACGAAATTTGAGAGGCGCCAGGAGTGC 2512
Db ||||||||||||||||||||||||||||||||||| 771
761 ThrHisGluPheGluArgAlaProArgSerVal 771

RESULT 6
PCT-US94-10151A-54
; Sequence 54, Application PC/TUS9410151A
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: The Semaphorin Gene Family
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/10151A
; FILING DATE: 13-SEP-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: FP-58750-PC/RAO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299 FHT UR
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 771 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US94-10151A-54

Alignment Scores:
Pred. No.: 0 Length: 771
Score: 771.00 Matches: 771
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 86.15% Indels: 0
DB: 5 Gaps: 0

US-09-774-490-1 (1-2709) x PCT-US94-10151A-54 (1-771)

QY 200 ATGGGCTGGTTAACTAGGATTGCTCTTTCTGGGAGTATTACTTACAGCAAGCA 259
Db 1 MetGlyTrpLeuThrArgIleValCysLeuPheTrpGlyValLeuLeuThrAlaArgAla 20
QY 260 AACTATCAGATGGGAGCAACAAATGTGCCAGGCTGAATATTCCTACAAAGAAATGTG 319
Db 21 AsnTyrGluAsnGlyLysAsnValProArgLeuLysLeuSerTyrLysGluMetLeu 40
QY 320 GAATCCAAATGTGATCACTTTCAATGCTTGGCCACAGCTCCAGTTATCATACCTTC 379
Db 41 GluSerAsnValIleThrPheAsnGlyLeuAlaAsnSerSerTyrHisThrPhe 60
QY 380 CTTTTCGATCAGGAACGGAGTGGCTGTATGTGGAGCAAGGATCAATATTTTCATTC 439
Db 61 LeuLeuAspGluArgSerArgLeuTyrValGlyAlaLysAspHisIlePheSerPhe 80
QY 440 GACCTGGTAAATATCAAGGATTTTCAAGATGTGTGGCCAGTATCTTACACCAAGAGA 499
Db 81 AspLeuValAsnIleLysAspPheGlnLysIleValTrpProValSerTyrThrArg 100

QY 500 GATGAATGCAAGTGGCTGGAAAAGACATCTCTGAAAGAAATGTCTAATTTTCATCAAGTGA 559
Db ||||||||||||||||||||||||||||||||||| 120
101 AspGluCysLeuTrpAlaGlyLysAspIleLeuLysGluCysAlaAsnPheIleLysVal 120
QY 560 CTTAAGGCATATTAATCAGACTCTCTGTAGCTGTGGAAACGGGGCTTTTCATCAATTT 619
Db ||||||||||||||||||||||||||||||||||| 140
121 LeuLysAlaTyrAsnGlnThrHisLeuTyrAlaCysGlyThrGlyAlaPheHisProIle 140
QY 620 TGCACCTACATTTGAAATTTGACATCATCTCTGAGGACAATATTTTAACTGGAGAACTCA 679
Db ||||||||||||||||||||||||||||||||||| 160
141 CysThrTyrIleGluIleGlyHisHisProGluAspAsnIlePheLysLeuGluAsnSer 160
QY 680 CATTTTAAACCGCGCTGGAGAGTCCATATGACCTTAAGCTGTCTGACAGCATCCCTTT 739
Db ||||||||||||||||||||||||||||||||||| 180
161 HisPheGluAsnGlyArgGlyLysSerProTyrAspProLysLeuLeuThrAlaSerLeu 180
QY 740 TTAATAGATGGACAATTACTCTGGAATGCGAGCTGATTTTATGGGGCAGACTTTGCT 799
Db ||||||||||||||||||||||||||||||||||| 200
181 LeuIleAspGlyGluLeuTyrSerGlyThrAlaAspPheMetGlyArgAspPheAla 200
QY 800 ATCTTCCGAACCTCTTGGGCACCAACCACCAATCAGACAGACAGCATGATTCACGGTGG 859
Db ||||||||||||||||||||||||||||||||||| 220
201 IlePheArgThrLeuGlyHisHisProIleArgThrGluGlnHisAspSerArgTyr 220
QY 860 CTCATGATCCAAAGTTCATTAGTGGCCACCTCATCTCAGAGAGTGCACATCTCTGAGAT 919
Db ||||||||||||||||||||||||||||||||||| 240
221 LeuAsnAspProLysPheIleSerAlaHisLeuIleSerGluSerAspAsnProGluAsp 240
QY 920 GACAAAGTATATCTTTTCTCCGTGAAATGCAATAGATGGAGAACACTCTGAAAAGCT 979
Db ||||||||||||||||||||||||||||||||||| 260
241 AspLysValTyrPhePheArgGluAsnAlaIleAspGlyGluHisSerGlyLysAla 260
QY 980 ACTCAGCTAGATAGTTCAGATATCAAGAAATGACTTTGGAGGGCACAGAACTCTGGTG 1039
Db ||||||||||||||||||||||||||||||||||| 280
261 ThrHisAlaArgIleGlyGlnIleCysLysAsnAspPheGlyHisArgSerLeuVal 280
QY 1040 AATAAATGGACAACTTCTCAAAGCTCGTCTCATTTGCTCAGTGCAGGTCCAAATGGC 1099
Db ||||||||||||||||||||||||||||||||||| 300
281 AsnLysTrpThrThrPheLeuLysAlaArgLeuIleCysSerValProGlyProAsnGly 300
QY 1100 ATTGACACTCATTTTGTATGAACGCGAGGTATCTCTAATGAACCTTTAAAGATCCTAAA 1159
Db ||||||||||||||||||||||||||||||||||| 320
301 IleAspThrHisPheAspGluLeuGlnAspValPheLeuMetAsnPheLysAspProLys 320
QY 1160 AATCCAGTTGTATATGAGTGTGTACACTTCCAGTAAACATTTTCAAGGGATCAGCGCTG 1219
Db ||||||||||||||||||||||||||||||||||| 340
321 AsnProValValTyrGlyValPheThrThrSerSerAsnIlePheLysGlySerAlaVal 340
QY 1220 TGTATGTATAGCATGATGTGAGAAAGGCTTCTCTGGTCCATATGCCACAGGAT 1279
Db ||||||||||||||||||||||||||||||||||| 360
341 CysMetTyrSerMetSerAspValArgArgValPheLeuGlyProTyrAlaHisArgAsp 360
QY 1280 GGACCCCAACTATCAATGGGTGCTTATCAAGGAAGAGTCCCTTATCAGCGCCAGGAACT 1339
Db ||||||||||||||||||||||||||||||||||| 380
361 GlyProAsnTyrGlnTrpValProTyrGlnGlyArgValProTyrProArgProGlyThr 380
QY 1340 TGTCACAGCAAAACATTTGGTGGTGTGTGACTTCACAAAGGACCTTCTGTATGATGTATA 1399
Db ||||||||||||||||||||||||||||||||||| 400
381 CysProSerLysThrPheGlyGlyPheAspSerThrLysAspLeuProAspAspValIle 400
QY 1400 ACCTTTTCCAAAGAAGTTCATCCAGCCATGTCAATCCAGTGTTCCTATGAAACAATCGCCCA 1459
Db ||||||||||||||||||||||||||||||||||| 420
401 ThrPheAlaArgSerHisProAlaMetTyrAsnProValPheProMetAsnAsnArgPro 420
QY 1460 ATAGTGATCAAAACGGATGTAAATTTATCATTTTACACAAATTCGTCTAGACCGAGTGGAT 1519
Db ||||||||||||||||||||||||||||||||||| 440
421 IleValIleLysThrAspValAsnTyrGlnPheThrGlnIleValValAspArgValAsp 440
QY 1520 GCAGAAATCGACAGATGATGTTATGTTTATCGGAACAGATGTGGGACCGTCTTCTTAAA 1579
Db ||||||||||||||||||||||||||||||||||| 460
441 AlaGluAspGlyGlnTyrAspValMetPheIleGlyThrAspValGlyThrValLeuLys 460
QY 1580 GTAGTTTCAATTCCTAAGGAGACTTGTGTATGATTTTAGAAGAGGTCTGTGGAGAAATG 1639

```
Db 461 ValValSerIleProLysGluThrTrpTyrAspLeuGluValLeuLeuGluMet 480
Qy 1640 ACAGTTTTTCGGACCGACTGCTATTTCCAGCAATGGAGCTTCCACTAAGACGACAA 1699
Db 481 ThrValPheArgGluProThrAlaIleSerAlaMetGluLeuSerThrLysGlnGln 500
Qy 1700 CTATATATGGTTCACCGCTGGGTTGCCAGCTCCCTTTACACCGGTGTGATATTAC 1759
Db 501 LeuTyrIleGlySerThrAlaGlyValAlaGlnLeuProLeuHisArgCysAspIleTyr 520
Qy 1760 GGGAAAGCGTGTGCTAGCTGTGCTCGCCGAGACCTTACTGCTGGTGGTGTCT 1819
Db 521 GlyLysAlaCysAlaGluCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlySer 540
Qy 1820 GCATGTTCTCGTATTTCCCACTGCAAGAGAGCGCAAGACGACAGATATAAGAAAT 1879
Db 541 AlaCysSerArgTyrPheProThrAlaLysArgArgThrArgGlnAspIleArgAsn 560
Qy 1880 GGAGACCCACTGACTACTGTTTCAGACTTACACCATGATATACCATGGCCAGCCCT 1939
Db 561 GlyAspProLeuThrHisCysSerAspLeuHisAspAsnHisGlyHisSerPro 580
Qy 1940 CAAGAGAGAAATCATCTATGGTGTAGAGTAATAGTACACATTTTGGAAATGCGACG 1999
Db 581 GluGluArgIleIleTyrGlyValGluAsnSerSerThrPheLeuGluCysSerProLys 600
Qy 2000 TCGCAGAGCGCTGGTCTATTGGCAATTCAGAGGGGAAATGAAGAGCGGAAAGAAG 2059
Db 601 SerGlnArgAlaLeuValTyrTrpGlnPheGlnArgArgAsnGluGluArgLysGlu 620
Qy 2060 ATCAGAGTGGATGATCATATCATCAGACAGATCARGGCTTCTGCTACGTAGTCTCAA 2119
Db 621 IleArgValAspAspHisIleIleArgThrAspGlnGlyLeuLeuLeuArgSerLeuGln 640
Qy 2120 CAGAGGATTCAGGCAATTAACCTCTGCCATCGGTGGAACATGGGTTTCATACAACTCTT 2179
Db 641 GlnLysAspSerGlyAsnTyrLeuCysHisAlaValGluHisGlyPheIleGlnThrLeu 660
Qy 2180 CTTAAGTTAACCTGGAAGTCAATTCAGACAGACATTTGGAGAACTTCTTCATAAGAT 2239
Db 661 LeuLysValThrLeuGluValIleAspThrGluHisLeuGluGluLeuHisLysAsp 680
Qy 2240 GATGATGAGATGGCTCTAAGACCAAGAAATGTCCATAGCATGACACCTAGCGCAAG 2299
Db 681 AspAspGlyAspGlySerLysThrLysGluMetSerAsnSerMetThrProSerGlnLys 700
Qy 2300 GTCTGGTACAGAGCTTCATGAGCTCATCAACACCCCAATCTCAACAGATGGATGAG 2359
Db 701 ValTrpTyrArgAspPheMetGlnLeuIleAsnHisProAsnLeuAsnThrMetAspGlu 720
Qy 2360 TTCTGTGACAAAGTTTGAAGAGGACCGAAGAAACAACTCGCGCAAGCCAGGACATACC 2419
Db 721 PheCysGluGlnValTrpLysArgAspArgLysGlnArgGlnArgProGlyHisThr 740
Qy 2420 CCAGGGAACAGTAAACAATGGAAGCACTTACAAGAAATATAAGAAAGTGAACAGGAGG 2479
Db 741 ProGlyAsnSerAsnLysTrpLysHisLeuGlnGluAsnLysLysGlyArgAsnArg 760
Qy 2480 ACCACGATTTGAGAGCGCCACCGAGGTCTC 2512
Db 761 ThrHisGluPheGluArgAlaProArgSerVal 771
```

RESULT 7

```
US-08-556-422A-3
; Sequence 3, Application US/08556422A
; Patent No. 6576754
; GENERAL INFORMATION:
; APPLICANT: HALL, Kathryn T.
; APPLICANT: FREEMAN, Gordon J.
; APPLICANT: SCHULTZE, Joachim L.
; APPLICANT: BOUSSIOTIS, Vassiliki
; APPLICANT: NADLER, Lee M.
```

```
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING CD100 MOLECULES
; FILE REFERENCE: DFN-005CPA2
; CURRENT APPLICATION NUMBER: US/08/556,422A
; CURRENT FILING DATE: 1995-11-09
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 655
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-556-422A-3
```

```
Alignment Scores:
Pred. No.: 0 Length: 655
Score: 655.00 Matches: 655
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 73.18% Indels: 0
DB: 4 Gaps: 0
```

US-09-774-490-1 (1-2709) x US-08-556-422A-3 (1-655)

```
Qy 200 ATGGGCTGTTAACTAGGATTGTCTCTTTCTGGGAGTATTACTTACAGCAAGACA 259
Db 1 MetGlyTyrLeuThrArgIleValCysLeuPheTrpGlyValLeuLeuThrAlaArgAla 20
Qy 260 AACTATCAGATGGGAAGCAATGTCGCAAGGCTGAAATATCTACAAAGAAATGTTG 319
Db 21 AsnTyrGlnAsnGlyLysAsnAsnValProArgLeuLysLeuSerTyrLysGluMetLeu 40
Qy 320 GAATCAACAATGTGATCATTTCATATGCTTGGCCAAAGCAGCTCCAGTTATCATACCTTC 379
Db 41 GluSerAsnAsnValIleThrPheAsnGlyLeuAlaAsnSerSerTyrHisThrPhe 60
Qy 380 CTTTGTGATGAGGAACGAGTAGGCTGTATGTTGGAGCAAGGATCACATATTTTCATTC 439
Db 61 LeuLeuAspGluGluArgSerArgLeuTyrValGlyAlaLysAspHisIlePheSerPhe 80
Qy 440 GACCTGTTTAAATATCAAGGATTTTCAAAAGATTTGTGTCGCGCATGATCTTACACCAAGA 499
Db 81 AspLeuValAsnIleLysAspPheGlnLysIleValTrpProValSerTyrThrArgArg 100
Qy 500 GATGAATCAATGGCTGGGAAAAGACATCTCTGAAGAAGATGTGCTAAATTTTCATCAGGTA 559
Db 101 AspGluCysLysTrpAlaGlyLysAspIleLeuLysGluCysAlaAsnPheIleLysVal 120
Qy 560 CTTAAGGCATATAATCAGACTCATTGTACGCTCTGGAACGGGGCTTTTCATCCAATT 619
Db 121 LeuLysAlaTyrAsnGlnThrHisLeuTyrAlaCysGlyThrGlyAlaPheHisProIle 140
Qy 620 TGCACCTACATTTGAAATTTGGACATCATCTGAGGACAATATTTTAACTGAGGAACATCA 679
Db 141 CysThrTyrIleGluIleGlyHisIleProGluAspAsnIlePheLysLeuGluAsnSer 160
Qy 680 CATTTTGAAGACGGCGTGGGAGAGTCCATATGACCTTACCTGCTGACAGCATCCCTTG 739
Db 161 HisPheGluAsnGlyArgGlyLysSerProTyrAspProLysLeuLeuThrAlaSerLeu 180
Qy 740 TTAATAGATGGAGAATTATATCTCTGAAACTGAGCTGATTTTATGGGCGAGACTTCTCT 799
Db 181 LeuIleAspGlyGluLeuTyrSerGlyThrAlaAlaAspPheMetGlyArgAspPheAla 200
Qy 800 ATCTTCGGAACCTTTGGGCAACCAACCAATCAGACAGACAGCAGCATGATTCAGGTTG 859
Db 201 IlePheArgThrLeuGlyHisHisIleSerProIleArgThrGluGlnHisAspSerArgTrp 220
Qy 860 CTCATATGATCCAAAGTTCATTAGTCCCACTCTCATCTCAGAGAGTGACAACTCTGGAAGAT 919
Db 221 LeuAsnAspProLysPheIleSerAlaHisLeuIleSerGluSerAspAsnProGluAsp 240
Qy 920 GACAAAGTATATCTTTTCTTCGTTGAAAATGAATAGATGAGAAACATCTCGGAAAGCT 979
Db 241 AspLysValTyrPhePheArgGluAsnAlaIleAspGlyGluHisSerGlyLysAla 260
```

QY 980 ACTCAGCTAGATAGTTCAGATATGCAAGATGACITTTGGAGGGCACAGAAGTCTGGT 1039
Db 261 ThrHisAlaAaGllleGlyGlnIleCysLysAsnAspPheGlyGlyHisArgSerLeuVal 280
QY 1040 AATAAATGGACAACATTCCTCAAGCTCGTCTGATTTGCTCAGTGCAGAGTCCAAATGGC 1099
Db 281 AsnLysTrpThrThrPheLeuLeuAlaArgLeuIleCysSerValProGlyProAsnGly 300
QY 1100 ATTGACACTCATTTTGATGAACTGCAGGATGATTTCTTAATGAACCTTTAAAGATCCTAAA 1159
Db 301 IleAspThrHisPheAspGluLeuGlnAspValPheLeuMetAsnPheLysAspProLys 320
QY 1160 AATCAGTTGATATGGAGTGTTCAGACTTCCAGTACACATTTCAAGGATCAGCCGTG 1219
Db 321 AsnProValValTyrGlyValPheThrThrSerSerAsnIlePheLysGlySerAlaVal 340
QY 1220 TGTATGTATACATGATGATGTGAGAGGTGTTCTTGTCATATGCCACAGAGAT 1279
Db 341 CysMetTyrSerMetSerAspValArgArgValPheLeuGlyProTyrAlaHisArgAsp 360
QY 1280 GGACCCAACTATCAATGGTGCCTTATCAAGGAAGAGTCCCTTATCCAGCCGCGAGAACT 1339
Db 361 GlyProAsnTyrGlnTrpValProTyrGlnGlyArgValProTyrProArgProGlyThr 380
QY 1340 TGTCACCAAAACATTTGGTGGTTTTCACCTCAAGAGGACCTTCCTGATGATTTATA 1399
Db 381 CysProSerLysThrPheGlyGlyPheAspSerThrLysAspLeuProAspAspValIle 400
QY 1400 ACCTTTGCAAGAAGTCATCCAGCCATGACAACTCAGTGTTCCTATCAACAATCGCCCA 1459
Db 401 ThrPheAlaAaGSerHisProAlaMetTyrAsnProValPheProMetAsnAsnArgPro 420
QY 1460 ATAGTGATCAAAACCGATGTAATATCAATTAACAATTCGATGATGATGATGAT 1519
Db 421 IleValIleLysThrAspValAsnTyrGlnPheThrGlnIleValValAspArgValAsp 440
QY 1520 CGAGAGATGACACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1579
Db 441 AlaGluAspGlyGlnTyrAspValMetPheIleGlyThrAspValGlyThrValLeuLys 460
QY 1580 GTAGTTCAATTCCTAAGGAGACTGGTATGATGATGATGATGATGATGATGATGATGAT 1639
Db 461 ValValSerIleProLysGluThrTrpTyrAspLeuGluValLeuLeuGluGluMet 480
QY 1640 ACAGTTTTCGGAAACCACTGCTATTTCCAGCAATGAGCTTCCACTAAGCAGACAA 1699
Db 481 ThrValPheArgGluProThrAlaIleSerAlaMetGluLeuSerThrLysGlnGln 500
QY 1700 CTATATATTGTTCAACGGCTGGGGTTCACAGCTCCCTTTACACCGGTGTGATATTAC 1759
Db 501 LeuTyrIleGlySerThrAlaGlyValAlaGlnLeuProLeuHisArgCysAspIleTyr 520
QY 1760 GGAAGAAGCGTGTGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1819
Db 521 GlyLysAlaCysAlaGluCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlySer 540
QY 1820 GCATGTTCTCGCTATTTTCCACTCCAAAGAGCCCAAGACGACAGATATAGAAAT 1879
Db 541 AlaCysSerArgTyrPheProThrAlaLysArgArgThrArgGlnAspIleArgAsn 560
QY 1880 GGAGACCCACTGACTCAGTGTTCAGACTTACACCATGATATACCATGCGCCACAGCCCT 1939
Db 561 GlyAspProLeuThrHisCysSerAspLeuHisAspAsnHisHisGlyHisSerPro 580
QY 1940 GAAGAGAGATCATCTATGCTGTAGAGATAGTACACATTTTGGATGAGTCCGAG 1999
Db 581 GluGluArgIleIleTyrGlyValGluAsnSerSerThrPheLeuGluCysSerProLys 600
QY 2000 TGCAGAGAGCCCTGCTGCTATTTGGCAATTTCCAGAGCGCAATTAAGAGCGAAAGAGAG 2059
Db 601 SerGlnArgAlaLeuValTyrTrpGlnPheGlnArgAsnGluGluArgLysGluGlu 620

QY 2060 ATCAGAGTGGATCATATCATATCATAGGACAGATCAAGGCTTCTGCTAGTGTCTACAA 2119
Db 621 IleArgValAspAspHisIleIleArgThrAspGlnGlyLeuLeuLeuArgSerLeuGln 640
QY 2120 CAGAAGGATTCAGGCAATTACCTCTGCCATGCGTGGAAACATGGG 2164
Db 641 GlnLysAspSerGlyAsnTyrLeuCysHisAlaValGluHisGly 655
RESULT 8
US-08-136-922-2
: Sequence 2, Application US/08136922
: Patent No. 5416197
: GENERAL INFORMATION:
: APPLICANT: Raper, Jonathan A.
: APPLICANT: Luo, Yuling
: TITLE OF INVENTION: Compositions Which Regulate Neural
: TITLE OF INVENTION: Regeneration and Methods of Making and Using the Same
: NUMBER OF SEQUENCES: 2
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
: ADDRESSEE: No. 5416197r1s
: STREET: One Liberty Place
: CITY: Philadelphia
: STATE: PA
: COUNTRY: USA
: ZIP: 19103
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/136,922
: FILING DATE:
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Deluca, Mark
: REGISTRATION NUMBER: 33,229
: REFERENCE/DOCKET NUMBER: UPN-1428
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 215-568-3100
: TELEFAX: 215-568-3439
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 477 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-08-136-922-2
Alignment Scores:
Pred. No.: 0 Length: 477
Score: 434.00 Matches: 434
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 48.49% Indels: 0
DB: 1 Gaps: 0
US-09-774-490-1 (1-2709) x US-08-136-922-2 (1-477)
QY 905 GACAATCCTCAAGATGACAAAGTATACTTTTCTTCGTGMAAATGCAATAGTGCAGAA 964
Db 4 AspAsnProGluAspAspLysValTyrPhePheArgGluAsnAlaIleAspGlyGlu 23
QY 965 CACTCTGGAAAAGCTACTCAGCTAGATAGGTGAGTATGCAAGAAATGACTTTGGAGGG 1024
Db 24 HisSerGlyLysAlaThrHisAlaAaGllleGlyGlnIleCysLysAsnAspPheGlyGly 43
QY 1025 CACAGAAGTCTGTGTAATAAATGCAACAATTCTCTCAAAGCTCTGATTCTCTCAGTG 1084
Db 44 HisArgSerLeuValAsnLysTrpThrThrPheLeuLysAlaArgLeuIleCysSerVal 63
QY 1085 CCAGGTCCTCAATGGCATGTGACACTCATTTTGTATGATGAATCGCAGGATGATTTCTTCAATGAAC 1144

Db 64 ProGlyProAsnGlyIleAspThrHisPheAspGluLeuGlnAspValPheLeuMetAsn 83
 1145 TTTAAAGATCTTAAATCCAGTGTATATGAGTGTATACGACTCCAGTACATTTTC 1204
 Db 84 PheLysAspProLysAsnProValValTyGlyValPheThrThrSerSerAsnIlePhe 103
 1205 AAGGATCAGCGGTGTGTATATAGCATGATGATGAGAGGGTGTTCCTTGTTCCA 1264
 Db 104 LysGlySerAlaValCysMetTySerMetSerAspValArgValPheLeuGlyPro 123
 1265 TATGCCACAGGATGAGCCCAATCATCATGAGTGTGCTTATCAGGAAGAGTCCCTAT 1324
 Db 124 TyrAlaHisArgAspGlyProAsnTyGlnTrpValProTyGlnGlyArgValProTy 143
 1325 CCAGGCCAGGAATGTGCCAGCAAAACATTTGGTGGTTTGTACTCTACAAAGGACCTT 1384
 Db 144 ProArgProGlyThrCysProSerLysThrPheGlyGlyPheAspSerThrLysAspLeu 163
 1385 CCTGATGATGTATAACCTTTGCAAGAGTCAATCCAGCCATGTACATCCAGTGTTCCT 1444
 Db 164 ProAspAspValIleThrPheAlaArgSerHisProAlaMetTyAsnProValPhePro 183
 1445 ATGACATCCCAATGATGATCAAAACGATGATTAATTAATCAATTTACAAATTTGTC 1504
 Db 184 MetAsnAsnArgProIleValIleLysThrAspValAsnTyGlnPheThrGlnIleVal 203
 1505 GTAGACCGAGTGGATGAGAGATGAGATGATGATGATGATGATGATGATGATGATG 1564
 Db 204 ValAspArgValAspAlaGluAspGlyGlnTyAspValMetPheIleGlyThrAspVal 223
 1565 GGGACCGTCTTAAAGTATGTTCAATTCCTAAGAGAGCTGGTATGATGATGATGATG 1624
 Db 224 GlyThrValLeuLysValIleSerIleProLysGluThrTrpTyAspLeuGluGluVal 243
 1625 CTGCTGGAAGAAATGACAGTGTTCGGGAACCGAGTCTATTTTCCAGCAATGGAGCTTCC 1684
 Db 244 LeuLeuGluGluMetThrValPheArgGluProThrAlaIleSerAlaMetGluLeuSer 263
 1685 ACTAAGCAGCAACATATATATGTTTCAAGCGTGGGTGGCCAGCTCCCTTTACAC 1744
 Db 264 ThrLysGlnGlnLeuTyIleGlySerThrAlaGlyValAlaGlnLeuProLeuHis 283
 1745 CGGTGTATATTTAGGGAAGAGTGTCTCAGTGTTCCTCGCCGAGACCCCTTACTGT 1804
 Db 284 ArgCysAspIleTyGlyLysAlaCysAlaGluCysCysLeuAlaArgAspProTyCys 303
 1805 GCTTGGGATGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1864
 Db 304 AlaTrpAspGlySerAlaCysSerArgTyPheProThrAlaLysArgGlyThrArg 323
 1865 CAAGATATAGAAATGAGAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1924
 Db 324 GlnAspIleArgGlnGlyAspProLeuThrHisCysSerAspLeuHisAspAsnHis 343
 1925 CATGCCACAGCCCTGAGAGAGATCATCATCATCATCATCATCATCATCATCATCATCAT 1984
 Db 344 HisGlyHisSerProGluGluArgIleIleTyGlyValGluAsnSerSerThrPheLeu 363
 1985 GAATGATGCAAGTCCAGAGAGCGTGTCTATTTGGCAATTCAGAGCGCAATGAA 2044
 Db 364 GluCysSerProLysSerGlnArgAlaLeuValTyTrpGlnPheGlnArgGlnGlu 383
 2045 CAGCGAAAGAGAGATCAGAGTGGATCATCATCATCATCATCATCATCATCATCATCATCAT 2104
 Db 384 GluArgLysGluGluIleArgValAspAspHisIleIleArgThrAspGlnGlyLeuLeu 403
 2105 CTACGTAGTCTACAAACAGAGATTCAGGCAATTTACCTCTGCGATGCGGTGGACATGGG 2164
 Db 404 LeuArgSerLeuGlnGlnLysAspSerGlyAsnTyLeuCysHisAlaValGluHisGly 423
 2165 TTACATCAAACTCTTCTTAAAGTAACTGGAAGTCAATTGAC 2206

Db 424 PheIleGlnThrLeuLeuLysValThrLeuGluValIleAsp 437
 RESULT 9
 US-09-308-179B-1
 ; Sequence 1, Application US/09308179B
 ; Patent No. 6436669
 ; GENERAL INFORMATION:
 ; APPLICANT: INAGAKI, Shinobu
 ; APPLICANT: FURUYAMA, Tatsuo
 ; TITLE OF INVENTION: NOVEL SEMAPHORIN GENES (I)
 ; FILE REFERENCE: 0020-4562P
 ; CURRENT APPLICATION NUMBER: US/09/308,179B
 ; CURRENT FILING DATE: 1999-05-14
 ; PRIOR APPLICATION NUMBER: PCT/JP97/04111
 ; PRIOR FILING DATE: 1997-11-12
 ; PRIOR APPLICATION NUMBER: JAPAN 321068/1996
 ; PRIOR FILING DATE: 1996-11-15
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 775
 ; TYPE: PRT
 ; ORGANISM: Mus sp.
 US-09-308-179B-1
 Alignment Scores:
 Pred. No.: 0.000703 Length: 775
 Score: 13.00 Matches: 13
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.45% Indels: 0
 DB: 4 Gaps: 0
 US-09-774-490-1 (1-2709) x US-09-308-179B-1 (1-775)
 QY 1778 TGTTCCTCGCCGAGACCCCTTACTGTCTGCGATGGT 1816
 Db 529 CysCysLeuAlaArgProTyCysAlaTrpAspGly 541
 RESULT 10
 US-09-041-236-4
 ; Sequence 4, Application US/09041236
 ; Patent No. 6225285
 ; GENERAL INFORMATION:
 ; APPLICANT: Luo, Yuling
 ; APPLICANT: Xiomei, Xu
 ; TITLE OF INVENTION: Semaphorin KI
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSER: SCIENCE & TECHNOLOGY LAW GROUP
 ; STREET: 75 DENISE DRIVE
 ; CITY: HILLSBOROUGH
 ; STATE: CALIFORNIA
 ; COUNTRY: USA
 ; ZIP: 94010
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA: US/09/041,236
 ; FILING DATE: March 11, 1998
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: OSMAN, RICHARD A
 ; REGISTRATION NUMBER: 36,627
 ; REFERENCE/DOCKET NUMBER: EXEL98-001
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (650) 343-4341
 ; TELEFAX: (650) 343-4342
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:

```
/ LENGTH: 606 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-09-041-236-4

Alignment Scores:
Pred. No.: 0.566 Length: 606
Score: 10.00 Matches: 10
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.12% Indels: 0
DB: 3 Gaps: 0

US-09-774-490-1 (1-2709) x US-09-041-236-4 (1-606)
QY 1043 AAATGACAACTTCTCAAGCTGCTG 1072
Db 255 LysTrpThrPheLeuLysAlaArgLeu 264

RESULT 11
US-09-771-467C-4
/ Sequence 4, Application US/09771467C
/ Patent No. 6583277
/ GENERAL INFORMATION:
/ APPLICANT: Luo, Yuling
/ TITLE OF INVENTION: Semaphorin K1 Polypeptides
/ NUMBER OF SEQUENCES: 4
/ CORRESPONDENCE ADDRESS:
/ ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP
/ STREET: 75 DENISE DRIVE
/ CITY: HILLSBOROUGH
/ STATE: CALIFORNIA
/ COUNTRY: USA
/ ZIP: 94010
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/771,467C
/ FILING DATE: 26-Jan-2001
/ CLASSIFICATION: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: OSMAN, RICHARD A
/ REGISTRATION NUMBER: 36,627
/ REFERENCE/DOCKET NUMBER: EXEL98-001
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (650) 343-4341
/ TELEFAX: (650) 343-4342
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 606 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-771-467C-4

Alignment Scores:
Pred. No.: 0.566 Length: 606
Score: 10.00 Matches: 10
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.12% Indels: 0
DB: 4 Gaps: 0

US-09-774-490-1 (1-2709) x US-09-771-467C-4 (1-606)
QY 1043 AAATGACAACTTCTCAAGCTGCTG 1072
Db 255 LysTrpThrPheLeuLysAlaArgLeu 264
```

```
Db 255 LysTrpThrPheLeuLysAlaArgLeu 264

RESULT 12
US-09-341-461-34
/ Sequence 34, Application US/09341461
/ Patent No. 6586389
/ GENERAL INFORMATION:
/ APPLICANT: Hammond, Timothy G.
/ APPLICANT: Verroust, Pierre J.
/ TITLE OF INVENTION: Cubilin Protein, DNA Sequences Encoding Cubilin
/ TITLE OF INVENTION: and Uses Thereof
/ FILE REFERENCE: D6148
/ CURRENT APPLICATION NUMBER: US/09/341,461
/ CURRENT FILING DATE: 2000-07-20
/ PRIOR APPLICATION NUMBER: PCI/US99/01259
/ PRIOR FILING DATE: 1999-01-21
/ NUMBER OF SEQ ID NOS: 40
/ SEQ ID NO 34
/ LENGTH: 112
/ TYPE: PRT
/ ORGANISM: human
/ FEATURE:
/ OTHER INFORMATION: amino acid sequence of CIs CUBI domain
US-09-341-461-34

Alignment Scores:
Pred. No.: 6.39 Length: 112
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.03% Indels: 0
DB: 4 Gaps: 0

US-09-774-490-1 (1-2709) x US-09-341-461-34 (1-112)
QY 151 TTGTGGGCGCAGAGATTCACAACT 125
Db 67 LeuCysGlyGlnArgSerSerAsnAsn 75

RESULT 13
US-08-556-422A-6
/ Sequence 6, Application US/08556422A
/ Patent No. 6576754
/ GENERAL INFORMATION:
/ APPLICANT: HALL, Kathryn T.
/ APPLICANT: FREEMAN, Gordon J.
/ APPLICANT: SCHULTZE Joachim L.
/ APPLICANT: BOUSIOTIS, Vassiliki
/ APPLICANT: NADLER, Lee M.
/ TITLE OF INVENTION: NUCLEIC ACIDS ENCODING CD100 MOLECULES
/ FILE REFERENCE: DFN-005CPA2
/ CURRENT APPLICATION NUMBER: US/08/556,422A
/ CURRENT FILING DATE: 1995-11-09
/ NUMBER OF SEQ ID NOS: 7
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 6
/ LENGTH: 295
/ TYPE: PRT
/ ORGANISM: Gallus gallus
US-08-556-422A-6

Alignment Scores:
Pred. No.: 5.68 Length: 295
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.01% Indels: 0
DB: 4 Gaps: 0

US-09-774-490-1 (1-2709) x US-08-556-422A-6 (1-295)
QY 1784 CTGCGCCGAGACCTTACTGTGTTGG 1810
Db 1784 CTGCGCCGAGACCTTACTGTGTTGG 1810
```

Thu Sep 23 08:54:05 2004

Search completed: September 21, 2004, 20:35:19
Job time : 97.5 secs

```
Db      287 LeuAlaArgAspProTyrCysAlaTrp 295

RESULT 14
US-08-556-422A-7
; Sequence 7, Application US/08556422A
; Patent No. 6576754
; GENERAL INFORMATION:
; APPLICANT: HALL, Kathryn T.
; APPLICANT: FREEMAN, Gordon J.
; APPLICANT: SCHULTZE, Joachim L.
; APPLICANT: BOUSSIOTIS, Vassiliki
; APPLICANT: NADLER, Lee M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING CD100 MOLECULES
; FILE REFERENCE: DEN-005CPA2
; CURRENT APPLICATION NUMBER: US/08/556,422A
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-556-422A-7

Alignment Scores:
Pred. No.:      5.44      Length:      425
Score:          9.00      Matches:      9
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match:      1.01%      Indels:      0
DB:              4          Gaps:      0

US-09-774-490-1 (1-2709) x US-08-556-422A-7 (1-425)

QY      1055 TTCTCAAGCTCGTCTGATTGTCA 1081
Db      104 PheLeuLysAlaArgLeuileCysSer 112

RESULT 15
US-08-556-422A-4
; Sequence 4, Application US/08556422A
; Patent No. 6576754
; GENERAL INFORMATION:
; APPLICANT: HALL, Kathryn T.
; APPLICANT: FREEMAN, Gordon J.
; APPLICANT: SCHULTZE, Joachim L.
; APPLICANT: BOUSSIOTIS, Vassiliki
; APPLICANT: NADLER, Lee M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING CD100 MOLECULES
; FILE REFERENCE: DEN-005CPA2
; CURRENT APPLICATION NUMBER: US/08/556,422A
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 607
; TYPE: PRT
; ORGANISM: Mus musculus
US-08-556-422A-4

Alignment Scores:
Pred. No.:      5.21      Length:      607
Score:          9.00      Matches:      9
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match:      1.01%      Indels:      0
DB:              4          Gaps:      0

US-09-774-490-1 (1-2709) x US-08-556-422A-4 (1-607)

QY      1784 CTCGCCGAGACCTTACTGCTTGG 1810
Db      483 LeuAlaArgAspProTyrCysAlaTrp 491
```

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 23, 2004, 04:46:07 ; Search time 2139 Seconds
(without alignments)

Title: US-09-774-490-1

Perfect score: 2709
Sequence: 1 aatcttttatttatcgatg.....agcttttttttctctaataacc 2709

Scoring table: OLIGO NUC

Gapop = 60.0 , Gapext = 60.0

Searched: 3337386 seqs. 2532474682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6674772

Minimum DB seq length: 0

Maximum DB seq length:	200000000
Maximum DB seq length:	200000000

Post-processing: Listing first 45 summaries

Database : Published Applications NA:*

```

1: /cgn2_6/ptodata/1/pubnpa/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/1/pubnpa/US07_PUBCOMB.seq.*
3: /cgn2_6/ptodata/1/pubnpa/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubnpa/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubnpa/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubnpa/US07_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubnpa/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/1/pubnpa/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubnpa/US09A_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubnpa/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubnpa/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/1/pubnpa/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/1/pubnpa/US09_NEW_PUB.seq.*
14: /cgn2_6/ptodata/1/pubnpa/US10A_PUBCOMB.seq.*
15: /cgn2_6/ptodata/1/pubnpa/US10B_PUBCOMB.seq.*
16: /cgn2_6/ptodata/1/pubnpa/US10C_PUBCOMB.seq.*
17: /cgn2_6/ptodata/1/pubnpa/US10_NEW_PUB.seq.*
18: /cgn2_6/ptodata/1/pubnpa/US60_NEW_PUB.seq.*
19: /cgn2_6/ptodata/1/pubnpa/US60_PUBCOMB.seq.*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2709	100.0	2709	9	US-09-774-490-1	Sequence 1, Appli
2	2517	92.9	2848	15	US-10-247-671-83	Sequence 83, Appl
3	2508	92.6	2530	15	US-10-097-340-283	Sequence 283, App
4	2508	92.6	2530	15	US-10-562-538-9	Sequence 9, Appli
5	2508	92.6	2601	15	US-10-067-632-53	Sequence 53, Appl
6	495	15.0	456	9	US-09-864-761-30992	Sequence 30992, A
7	303	11.2	354	9	US-09-932-217-736	Sequence 736, App
8	303	11.2	354	9	US-09-833-563-736	Sequence 736, App
9	303	11.2	354	14	US-10-025-380-736	Sequence 736, App
10	292	10.8	496	9	US-09-864-761-1444	Sequence 1444, A
C 11	161	5.9	164	15	US-10-029-386-18184	Sequence 18184, A
C 12	161	5.9	591	15	US-10-029-386-4484	Sequence 4484, Ap
C 13	160	5.9	172	9	US-09-864-761-27943	Sequence 27943, A
14	160	5.9	191	15	US-10-029-386-16491	Sequence 16491, A

C	15	160	5.9	484	9	US-09-864-761-11363	Sequence 11363, A	
		160	5.9	526	15	US-10-029-386-2791	Sequence 2791, A	
		160	5.9	526	15	US-10-029-386-2791	Sequence 2791, A	
		17	144	5.3	446	9	US-09-864-761-11810	Sequence 11810, A
		18	123	4.5	123	9	US-09-864-761-23831	Sequence 23831, A
C	19	122	4.5	123	9	US-09-864-761-6056	Sequence 6056, A	
		19	122	4.5	456	9	US-09-864-761-6056	Sequence 6056, A
		20	101	3.7	101	9	US-09-864-761-23893	Sequence 23893, A
C	21	71	2.6	2137	9	US-09-774-490-6	Sequence 6, Appli	
		21	2.6	2137	9	US-09-774-490-6	Sequence 238542, A	
		22	67	2.5	520	13	US-10-027-632-238542	Sequence 238542, A
		23	67	2.5	520	13	US-10-027-632-238543	Sequence 238543, A
		24	67	2.5	520	16	US-10-027-632-238542	Sequence 238542, A
		25	520	16	US-10-027-632-238543	Sequence 238543, A		
		26	60	2.2	60	10	US-09-908-975-15846	Sequence 15846, A
		27	50	1.8	50	16	US-10-131-827-4731	Sequence 4731, A
C	28	31	1.1	4661	9	US-09-897-006-10	Sequence 10, Appl	
		29	31	1.1	4661	10	US-09-897-511A-10	Sequence 10, Appl
		30	31	1.1	4661	13	US-10-397-079-10	Sequence 10, Appl
C	31	31	1.1	7160	8	US-08-786-531B-5	Sequence 5, Appli	
		32	31	1.1	7235	8	US-08-786-531B-6	Sequence 6, Appli
C	33	31	1.1	29	17	US-10-687-241-7	Sequence 7, Appli	
		34	26	1.0	1313	9	US-09-728-422-1	Sequence 1, Appli
C	35	25	0.9	25	17	US-10-687-241-2	Sequence 2, Appli	
		36	25	0.9	1400	9	US-09-774-490-5	Sequence 5, Appli
		37	24	0.9	24	17	US-10-687-241-1	Sequence 1, Appli
		38	24	0.9	485	10	US-09-814-353-12826	Sequence 1, Appli
		39	24	0.9	1665	13	US-10-424-599-82082	Sequence 82082, A
		40	24	0.9	1092	10	US-09-814-353-19094	Sequence 19094, A
		41	23	0.8	29	17	US-10-687-241-5	Sequence 5, Appli
C	42	23	0.8	175	13	US-09-990-747-24	Sequence 24, Appl	
		43	23	0.8	240	13	US-09-990-747-27	Sequence 27, Appl
C	44	23	0.8	287	13	US-09-990-747-18	Sequence 18, Appl	
		45	23	0.8	335	13	US-09-990-747-26	Sequence 26, Appl

ALIGNMENTS

```

RESULT 1
US-09-774-490-1
; Sequence 1, Application US/09774490
; Patent No. US20010034332A1
; GENERAL INFORMATION:
; APPLICANT: Jin, Shengfang
; TITLE OF INVENTION: RESISTANCE SEQUENCES AND USES THEREOF
; FILE REFERENCE: 07334-138001
; CURRENT APPLICATION NUMBER: US/09/774,490
; CURRENT FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: US 60/179,191
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2709
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-774-490-1

```

Query Match	100.0%;	Score 2709;	DB 9;	Length 2709;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 2709:	Conservative	0;	Mismatches	0;
	Indels	0;	Gaps	0;

1	AATCTTTATTTTATCGATGTTTAAAGACTTAGTAATCGATGCCAGCTCGAGGGGTGCG	60
1	AATCTTTTATTTTATCGATGTTTAAAGACTTAGTAATCGATGCCAGCTCGAGGGGTGCG	60
61	ACCCACGGTCCGGGAGTAGGTTGAGCTCGCCTGTTTCTCCCATTTGTCACCCAGTCTATTT	120
61	ACCCACGGTCCGGGAGTAGGTTGAGCTCGCCTGTTTCTCCCATTTGTCACCCAGTCTATTT	120
121	CCAGATTGTTTGAATCTTCTGGCCGCACAAATACAGGAAGGAAGACTTAAAGCAGCAAAAGG	180
121	CCAGATTGTTTGAATCTTCTGGCCGCACAAATACAGGAAGGAAGACTTAAAGCAGCAAAAGG	180
181	GACCTACAGCGCTGTCAGCATGGGCTGGTTAACTAGGAATTTGTCGTCTTTTCTGGGGAGT	240

D _b	181	GACCTACAGCGTCTGCAGCATGGGCTGGTTAACTAGGAATGTCTGTCTTTCTGGGAGT	240
Q _y	241	ATTACTTACGCAAGAGCAAATCATCAGAATGGGAAGAACAAATGTGCCAAGCTGAAATT	300
D _b	241	ATTACTTACGCAAGAGCAAATCATCAGAATGGGAAGAACAAATGTGCCAAGCTGAAATT	300
Q _y	301	ATCCTCAAAAGAAATGTGGAAATCCAAACATGTGATCACTTTCAATGGCTTGCCCAACAG	360
D _b	301	ATCCTCAAAAGAAATGTGGAAATCCAAACATGTGATCACTTTCAATGGCTTGCCCAACAG	360
Q _y	361	CTCCAGTTATCATACCTTCCTTTTGGATCAGGAACGGAGTAGGCTGTATGTTGGAGCAA	420
D _b	361	CTCCAGTTATCATACCTTCCTTTTGGATCAGGAACGGAGTAGGCTGTATGTTGGAGCAA	420
Q _y	421	GGATCATATTTTTTCATTCGACCTGGTTAATAACAAGGATTTTTCAAAAGATTGTGTGGCC	480
D _b	421	GGATCATATTTTTTCATTCGACCTGGTTAATAACAAGGATTTTTCAAAAGATTGTGTGGCC	480
Q _y	481	AGTATCTTACACAGAGAGATGAATGCAAGTGGCTGGAAAGACATCTGAAAAGATTG	540
D _b	481	AGTATCTTACACAGAGAGATGAATGCAAGTGGCTGGAAAGACATCTGAAAAGATTG	540
Q _y	541	TGCTAATTTTCATCAAGTACTTAAGGCATATATCAGATCTCACTGTACGCCCTGTGGAAC	600
D _b	541	TGCTAATTTTCATCAAGTACTTAAGGCATATATCAGATCTCACTGTACGCCCTGTGGAAC	600
Q _y	601	GGGGGCTTTTCATCCAATTTGCACCTACATGTGAAATGGAACATCATCTCGAGACAAATAT	660
D _b	601	GGGGGCTTTTCATCCAATTTGCACCTACATGTGAAATGGAACATCATCTCGAGACAAATAT	660
Q _y	661	TTTTTAAGCTGGAGNACTCACATTTTGGAAACGGCGGTGGGAAGAGTCCATATGACCCTAA	720
D _b	661	TTTTTAAGCTGGAGNACTCACATTTTGGAAACGGCGGTGGGAAGAGTCCATATGACCCTAA	720
Q _y	721	GCTGCTGACAGCATCCCCCTTTTAATAGATGAGAAATTAATACTCTGGAACCTCGAGCTGATTT	780
D _b	721	GCTGCTGACAGCATCCCCCTTTTAATAGATGAGAAATTAATACTCTGGAACCTCGAGCTGATTT	780
Q _y	781	TATGGGGCGAGACTTTGCTATCTTCGAACTCTTGGCACCCACCCCAATCAGGACAGA	840
D _b	781	TATGGGGCGAGACTTTGCTATCTTCGAACTCTTGGCACCCACCCCAATCAGGACAGA	840
Q _y	841	GCAGCATGANTCCAGGTGGCTCAATGATCAAAAGTTCATTAGTGGCCCACTCATCTCAGA	900
D _b	841	GCAGCATGANTCCAGGTGGCTCAATGATCAAAAGTTCATTAGTGGCCCACTCATCTCAGA	900
Q _y	901	GAGTGA CAATCTCGAAGATGACAAAGTATATCTTTCTCCGTGAAAATGCAATAGATGG	960
D _b	901	GAGTGA CAATCTCGAAGATGACAAAGTATATCTTTCTCCGTGAAAATGCAATAGATGG	960
Q _y	961	AGAACCTCTGGAAAAGCTACTCAGCGTAGAATAGGTTCAGATATGCAAGAAATGCACTTTGG	1020
D _b	961	AGAACCTCTGGAAAAGCTACTCAGCGTAGAATAGGTTCAGATATGCAAGAAATGCACTTTGG	1020
Q _y	1021	AGGSCACAGAAGTCTGTGTGAATAAATGGACAACATTCCTCAAAGCTGCTGATTTGCTC	1080
D _b	1021	AGGSCACAGAAGTCTGTGTGAATAAATGGACAACATTCCTCAAAGCTGCTGATTTGCTC	1080
Q _y	1081	AGTCCAGGTCCAAATGGCATGACACTCATTTTGTATGAGTCTGAGGATGATTTCTTAAT	1140
D _b	1081	AGTCCAGGTCCAAATGGCATGACACTCATTTTGTATGAGTCTGAGGATGATTTCTTAAT	1140
Q _y	1141	GAACTTTTAAAGATCCTAAAAATCCAGTTGTATATGGAGTGTTCAGACTTCCAGTAAACAT	1200
D _b	1141	GAACTTTTAAAGATCCTAAAAATCCAGTTGTATATGGAGTGTTCAGACTTCCAGTAAACAT	1200
Q _y	1201	TTTTCAAGGGATCAGCGGTGTATAGTATAGCATGAGTGTGAGAGAGGGTGTTCCTTGG	1260
D _b	1201	TTTTCAAGGGATCAGCGGTGTATAGTATAGCATGAGTGTGAGAGAGGGTGTTCCTTGG	1260
Q _y	1261	TCCATATGCCACAGGGATGACCCCAACTATCAATGGGTGCCCTTATCAAGGAAGAGTCCC	1320
D _b	1261	TCCATATGCCACAGGGATGACCCCAACTATCAATGGGTGCCCTTATCAAGGAAGAGTCCC	1320

1261	Db	TCCATATGCCACAGGGATGGACCCAACTATCAATGGGTGCCCTTATCAAGGAGAGTCCC	1321
1321	Qy	CTATCCACGCGCAGGAACTTGTCCCGACGAAAAATTTGGTGGTTTTGACTCTACAAGGA	1380
1321	Db	CTATCCACGCGCAGGAACTTGTCCCGACGAAAAATTTGGTGGTTTTGACTCTACAAGGA	1380
1381	Qy	CTTCTCTGATGATGTTATAACCTTTGCAAGAAGTCTATCCAGCCATGTACAATCCAGTGT	1440
1381	Db	CTTCTCTGATGATGTTATAACCTTTGCAAGAAGTCTATCCAGCCATGTACAATCCAGTGT	1440
1441	Qy	TCCTATGAAACAATCGCCCAATAGTGTCAAAAACGGATGTAAATTTTCAATTTTACAAAT	1500
1441	Db	TCCTATGAAACAATCGCCCAATAGTGTCAAAAACGGATGTAAATTTTCAATTTTACAAAT	1500
1501	Qy	TGTCGTAGACCGAGTGGATGCAGAGAATGACAGATATGATGTTATGTTTATCCGACAGA	1560
1501	Db	TGTCGTAGACCGAGTGGATGCAGAGAATGACAGATATGATGTTATGTTTATCCGACAGA	1560
1561	Qy	TGTTGGGACCGTTCTTAAAGTAGTTTTCAATTTCTTAAGGACACTTGGTATGATTTAGAAGA	1620
1561	Db	TGTTGGGACCGTTCTTAAAGTAGTTTTCAATTTCTTAAGGACACTTGGTATGATTTAGAAGA	1620
1621	Qy	GGTTCCTGCTGGGAAGAAATGACAGCTTTTTCGGGAACCGACTGCTATTTTCAGCAATGAGACT	1680
1621	Db	GGTTCCTGCTGGGAAGAAATGACAGCTTTTTCGGGAACCGACTGCTATTTTCAGCAATGAGACT	1680
1681	Qy	TTCCACTAAGCAGCAACACTATATATGTTTCAACGGCTGGGGTGTGCCCAGACTCCCTTT	1740
1681	Db	TTCCACTAAGCAGCAACACTATATATGTTTCAACGGCTGGGGTGTGCCCAGACTCCCTTT	1740
1741	Qy	ACACCGGTGTGATATTTACGGGAAGACGCTGCTGAGTGTGTGCTGCCCGAGACCCCTTA	1800
1741	Db	ACACCGGTGTGATATTTACGGGAAGACGCTGCTGAGTGTGTGCTGCCCGAGACCCCTTA	1800
1801	Qy	CTGTGCTTGGGATGGTTCCTCATGTTCTCGCTATTTTCCCACTGCAAGAGAGCGCACAG	1860
1801	Db	CTGTGCTTGGGATGGTTCCTCATGTTCTCGCTATTTTCCCACTGCAAGAGAGCGCACAG	1860
1861	Qy	ACGACAGATATTAAGAAATGGAGACCCACTGACTCACTGTTTCAGACTTACACCATGATAA	1920
1861	Db	ACGACAGATATTAAGAAATGGAGACCCACTGACTCACTGTTTCAGACTTACACCATGATAA	1920
1921	Qy	TCACCATGGCCACAGCCCTGAAGAGAAATCATCTATGTTGTGTAGAGAAATAGTAGCACATT	1980
1921	Db	TCACCATGGCCACAGCCCTGAAGAGAAATCATCTATGTTGTGTAGAGAAATAGTAGCACATT	1980
1981	Qy	TTTGGATGCAGTCCGAAAGTCGACAGAGCGCTGTCTATTGGCAATTCAGAGGCGCAAA	2040
1981	Db	TTTGGAAATGCAGTCCGAAAGTCGACAGAGCGCTGTCTATTGGCAATTCAGAGGCGCAAA	2040
2041	Qy	TGAAGACGCAAAAAGAGATCGAGTGGATGATCATATCATCAGGACAGATCAAGGCCT	2100
2041	Db	TGAAGACGCAAAAAGAGATCGAGTGGATGATCATATCATCAGGACAGATCAAGGCCT	2100
2101	Qy	TCTGCTACGTAGTCTACAAAGAGAGGATCAGGCAATTAACCTCTGCCATGCGGTGGAAACA	2160
2101	Db	TCTGCTACGTAGTCTACAAAGAGAGGATCAGGCAATTAACCTCTGCCATGCGGTGGAAACA	2160
2161	Qy	TGGGTTTCATACAAACTCTTCTTAAGGTAAACCTCGGAAGTCATTGCAACAGAGCAATTTGGA	2220
2161	Db	TGGGTTTCATACAAACTCTTCTTAAGGTAAACCTCGGAAGTCATTGCAACAGAGCAATTTGGA	2220
2221	Qy	AGAACTTCTTCAATAAGATGATGAGATGGCTCTTAAGACCAAGAAATGTCCTCAATAG	2280
2221	Db	AGAACTTCTTCAATAAGATGATGAGATGGCTCTTAAGACCAAGAAATGTCCTCAATAG	2280
2281	Qy	CATCACACCTAGCCAGAGAGGTCTCGTACAGAGACTTTCATGCAGCTCATCAACCCCAAA	2340
2281	Db	CATCACACCTAGCCAGAGAGGTCTCGTACAGAGACTTTCATGCAGCTCATCAACCCCAAA	2340
2341	Qy	TCTCAAACCGATGGATGAGTCTGTGAACAAAGTTTGGAAAGGACCGAAACACGTCG	2400
2341	Db	TCTCAAACCGATGGATGAGTCTGTGAACAAAGTTTGGAAAGGACCGAAACACGTCG	2400

Qy 2401 GCAAGGCCAGGACATACCCAGGGAACAGTAACAAATGAAGACACTTACAGAAATAA 2460
Db 2401 GCAAGGCCAGGACATACCCAGGGAACAGTAACAAATGAAGACACTTACAGAAATAA 2460
Qy 2461 GAAAGGTAGAAAACAGGAGGACCCAGCAATTTGAGAGGGCACCCAGGAGTGTCTGAGCTGC 2520
Db 2461 GAAAGGTAGAAAACAGGAGGACCCAGCAATTTGAGAGGGCACCCAGGAGTGTCTGAGCTGC 2520
Qy 2521 ATTACCTCTAGAAACCTCAACCAAGTAGAAGTTCCTAGACAAATCACTGGAACAAACAA 2580
Db 2521 ATTACCTCTAGAAACCTCAACCAAGTAGAAGTTCCTAGACAAATCACTGGAACAAACAA 2580
Qy 2581 TGCNATATAGATGACATTTTTCATGCAATATGTGATCTTTTACATGCTGGGAATTC 2640
Db 2581 TGCNATATAGATGACATTTTTCATGCAATATGTGATCTTTTACATGCTGGGAATTC 2640
Qy 2641 AGCTGAGTTCACCAATATATAAATTAATCAATGAGTAATCTTCTTAATAGGCTTTTTT 2700
Db 2641 AGCTGAGTTCACCAATATATAAATTAATCAATGAGTAATCTTCTTAATAGGCTTTTTT 2700
Qy 2701 CCTAATACC 2709
Db 2701 CCTAATACC 2709

RESULT 2
US-10-247-671-83
; Sequence 83, Application US/10247671
; Publication No. US20030194721A1
; GENERAL INFORMATION:
; APPLICANT: Mikita, Thomas
; APPLICANT: Shiffman, Dov
; APPLICANT: Porter, Gordon, J.
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED FOAM CELLS
; FILE REFERENCE: PA-0050 US
; CURRENT APPLICATION NUMBER: US/10/247,671
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: 60/323,784
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: PERL Program
; SEQ ID NO 83
; LENGTH: 2848
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030194721A1 1930967CB1
US-10-247-671-83

Query Match 92.9%; Score 2517; DB 15; Length 2848;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2517; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 193 CTGAGATGGCGTGGTTAACTAGGATGTCTGTCTTTCTGGGAGTATTACTTACAGC 252
Db 9 CTGAGATGGCGTGGTTAACTAGGATGTCTGTCTTTCTGGGAGTATTACTTACAGC 68

Qy 253 AAGAGCAACTATCAGATGGAGAACAAATGTCAGAGGTGAAATTCCTTACAAAGA 312
Db 69 AAGAGCAACTATCAGATGGAGAACAAATGTCAGAGGTGAAATTCCTTACAAAGA 128

Qy 313 AATGTTGGAATCCAAACATGTGATCACTTTCAATGGCTTGGCCAAAGCTCCAGTTATCA 372
Db 129 AATGTTGGAATCCAAACATGTGATCACTTTCAATGGCTTGGCCAAAGCTCCAGTTATCA 188

Qy 373 TACCTTCCTTTTGGATGAGGACCGAGTAGGCTGTATGTTGGAGCAAGGATCACATATT 432
Db 189 TACCTTCCTTTTGGATGAGGACCGAGTAGGCTGTATGTTGGAGCAAGGATCACATATT 248

Qy 433 TTCATTGCACTGGTTAATATCAAGGATTTTCAAAGATTTGTGTGGCCAGTATCTTACAC 492

Db 249 TTCAATTCGACCTGGTTAATATATCAAGGATTTTCAAAGATTTGTGTGGCCAGTATCTTACAC 308
Qy 493 CAGAAAGAGATGAATCAAGTGGCTTGGAAAAGACATCTCTGAAAGAAATGTCTAATTTTCAT 552
Db 309 CAGAAAGAGATGAATCAAGTGGCTTGGAAAAGACATCTCTGAAAGAAATGTCTAATTTTCAT 368
Qy 553 CAGAGTACTTAAGGATATATATCAGACTCACTTGTACGCTGTGAAACGGGGGCTTTTCA 612
Db 369 CAGAGTACTTAAGGATATATATCAGACTCACTTGTACGCTGTGAAACGGGGGCTTTTCA 428
Qy 613 TCCAAATTTGCACCTACATTTGAAATTTGAGACATCATCTCTGAGGACAAATATTTTAAAGCTGGA 672
Db 429 TCCAAATTTGCACCTACATTTGAAATTTGAGACATCATCTCTGAGGACAAATATTTTAAAGCTGGA 488
Qy 673 GAACTCAATTTTGAACACGGCCGTGGGAAGAGTCCATATGACCTTAAGTGTCTGACAGC 732
Db 489 GAACTCAATTTTGAACACGGCCGTGGGAAGAGTCCATATGACCTTAAGTGTCTGACAGC 548
Qy 733 ATCCCTTTTAAATAGATGAGAAATTAATCTCTGGAATCTCAGCTGATTTTATGGGGCGAGA 792
Db 549 ATCCCTTTTAAATAGATGAGAAATTAATCTCTGGAATCTCAGCTGATTTTATGGGGCGAGA 608
Qy 793 CTTTGTCTATCTTCGAACTCTTTGGGCAACACACCAATCAAGACAGAGAGCATGATTC 852
Db 609 CTTTGTCTATCTTCGAACTCTTTGGGCAACACACCAATCAAGACAGAGAGCATGATTC 668
Qy 853 CAGGTGGCTCATATGATCCAAAGTTTCATTTAGTGCACCTCATCTCAGAGAGTGACAATCC 912
Db 669 CAGGTGGCTCATATGATCCAAAGTTTCATTTAGTGCACCTCATCTCAGAGAGTGACAATCC 728
Qy 913 TGAAGATGACAAAGTATATCTTTTCTCCGTGAAATGCAATAGATGAGGAACACTCTGG 972
Db 729 TGAAGATGACAAAGTATATCTTTTCTCCGTGAAATGCAATAGATGAGGAACACTCTGG 788
Qy 973 AAAAGCTACTCAGCTAGAAATAGGTGAGATGCAAGATGACATTTTGAAGGACAGAG 1032
Db 789 AAAAGCTACTCAGCTAGAAATAGGTGAGATGCAAGATGACATTTTGAAGGACAGAG 848
Qy 1033 TCTGTGTAATAAATGGACAACTTCTCAAAGCTCGTCTGATTTTCTCAGTGCAGAGTCC 1092
Db 849 TCTGTGTAATAAATGGACAACTTCTCAAAGCTCGTCTGATTTTCTCAGTGCAGAGTCC 908
Qy 1093 AAATGGCATGTACATCTATTTTGTATGAACTGAGAGATGTATCTCTAATGAATTTTAAAGA 1152
Db 909 AAATGGCATGTACATCTATTTTGTATGAACTGAGAGATGTATCTCTAATGAATTTTAAAGA 968
Qy 1153 TCCTAAAATCCAGTGTATATGAGAGTGTACGACTTCCAGTACATTTTCAAGGGATC 1212
Db 969 TCCTAAAATCCAGTGTATATGAGAGTGTACGACTTCCAGTACATTTTCAAGGGATC 1028
Qy 1213 AGCCGTGTGTATGTATAGCATGAGTGTGAGAGGGTGTCTCTTGTCTCATATGCCCA 1272
Db 1029 AGCCGTGTGTATGTATAGCATGAGTGTGAGAGGGTGTCTCTTGTCTCATATGCCCA 1088
Qy 1273 CAGGATGAGACCAACTATCAATGGTGCCTTATCAAGGAAGTCCCTTATCCAGGCC 1332
Db 1089 CAGGATGAGACCAACTATCAATGGTGCCTTATCAAGGAAGTCCCTTATCCAGGCC 1148
Qy 1333 AGGAATCTTCCAGCAAAACATTTTGTGTTTGTGACTCTACAAAGGACCTTCTGTATGA 1392
Db 1149 AGGAATCTTCCAGCAAAACATTTTGTGTTTGTGACTCTACAAAGGACCTTCTGTATGA 1208
Qy 1393 TGTATAACCTTTGCAAGAGTCAATCCAGCCATGTACAAATCCAGTGTCTTATGAAACA 1452
Db 1209 TGTATAACCTTTGCAAGAGTCAATCCAGCCATGTACAAATCCAGTGTCTTATGAAACA 1268
Qy 1453 TCGCCCAATAGTATCAAAACGGATGTAATTTATCAATTTACAAAATTTCTGTAGACCG 1512
Db 1269 TCGCCCAATAGTATCAAAACGGATGTAATTTATCAATTTACAAAATTTCTGTAGACCG 1328
Qy 1513 AGTGGATGAGAGATGAGACATGATGTATGTTTATCGGAAACAGATGTTGGACCGT 1572

QY 433 TTCAATTCGACCTGGTTAATATCAAGGATTTTCAAAGATTTGTGTGGCCAGTATCTTACAC 492
 Db 249 TTCAATTCGACCTGGTTAATATCAAGGATTTTCAAAGATTTGTGTGGCCAGTATCTTACAC 308
 QY 493 CAGAAGAGATCAATGCAAGTGGCTGGAAAGACATCTGAAAGATGTGCTAATTTTCAT 552
 Db 309 CAGAAGAGATCAATGCAAGTGGCTGGAAAGACATCTGAAAGATGTGCTAATTTTCAT 368
 QY 553 CAAGGTACTTAAGGCATATAATCAAGCTCACTTTGACGCCGTGTGGAACGGGGGTTTTTCA 612
 Db 369 CAAGGTACTTAAGGCATATAATCAAGCTCACTTTGACGCCGTGTGGAACGGGGGTTTTTCA 428
 QY 613 TCCAAATTTGACCTACATTTGAAATTTGGACATCATCTTGGAGACATATATTTTAAGCTGGA 672
 Db 429 TCCAAATTTGACCTACATTTGAAATTTGGACATCATCTTGGAGACATATATTTTAAGCTGGA 488
 QY 673 GAACCTCACATTTTGAACCGCCCTGGGAAGAGTCCATATGACCCCTAAGCTGTGACAGC 732
 Db 489 GAACCTCACATTTTGAACCGCCCTGGGAAGAGTCCATATGACCCCTAAGCTGTGACAGC 548
 QY 733 ATCCCTTTTAATAGATGGAGATTTATCTCTGGAACTCTTGGAACTGCACTGATTTTATGGGCGAGA 792
 Db 549 ATCCCTTTTAATAGATGGAGATTTATCTCTGGAACTGCACTGATTTTATGGGCGAGA 608
 QY 793 CTTTGTCTATCTTCCGAACTCTTGGGACCAACCACCAATCAGGACAGACAGATGATTC 852
 Db 609 CTTTGTCTATCTTCCGAACTCTTGGGACCAACCACCAATCAGGACAGACAGATGATTC 668
 QY 853 CAGTGGCTCAATGATCAAAAGTTCAATTAGTGCCCACTCTATCTCAGAGAGTGACAAATCC 912
 Db 669 CAGTGGCTCAATGATCAAAAGTTCAATTAGTGCCCACTCTATCTCAGAGAGTGACAAATCC 728
 QY 913 TGAAGATGACAAAGTATATCTTTTCTTCCGTGAAATGCAATAGATGAGAAACACTCTGG 972
 Db 729 TGAAGATGACAAAGTATATCTTTTCTTCCGTGAAATGCAATAGATGAGAAACACTCTGG 788
 QY 973 AAAAGCTACTCACCTAGAATAGTTCAGATATGCAAGATGACCTTGGAGGGCACAGAAG 1032
 Db 789 AAAAGCTACTCACCTAGAATAGTTCAGATATGCAAGATGACCTTGGAGGGCACAGAAG 848
 QY 1033 TCTGGTGAATAAATGGACACATCTTCTCAAGCTCGTCTGATTTGCTCAGTGCCAGTCC 1092
 Db 849 TCTGGTGAATAAATGGACACATCTTCTCAAGCTCGTCTGATTTGCTCAGTGCCAGTCC 908
 QY 1093 AAATGGCATTGACACTCATTTTGTGAACTGCAGGATGATTCCTAATGAACCTTTAAAGA 1152
 Db 909 AAATGGCATTGACACTCATTTTGTGAACTGCAGGATGATTCCTAATGAACCTTTAAAGA 968
 QY 1153 TCCATAAAATCCAGTTGTATAGAGTGTGTTAAGACTTCCAGTAAACATTTTCAAGGGATC 1212
 Db 969 TCCATAAAATCCAGTTGTATAGAGTGTGTTAAGACTTCCAGTAAACATTTTCAAGGGATC 1028
 QY 1213 AGCCGTGTATGTATAGCATGATGTGAGAAAGGTGTCTCTTGGTCCATATGCCCA 1272
 Db 1029 AGCCGTGTATGTATAGCATGATGTGAGAAAGGTGTCTCTTGGTCCATATGCCCA 1088
 QY 1273 CAGGGATGGACCCCACTATCAATCGGTGCCCTTATCAAGGAAGAGTCCCTTATCCACGGCC 1332
 Db 1089 CAGGGATGGACCCCACTATCAATCGGTGCCCTTATCAAGGAAGAGTCCCTTATCCACGGCC 1148
 QY 1333 AGGAACCTGTCAGCAAGATTTGGTGGTTTGTGACTCTACAAAGACCTTCTCTATGA 1392
 Db 1149 AGGAACCTGTCAGCAAGATTTGGTGGTTTGTGACTCTACAAAGACCTTCTCTATGA 1208
 QY 1393 TGTATTAACTTTGCAAGAGATCTACAGGCATGTACAATCCAGTGTTCCTTATGAACA 1452
 Db 1209 TGTATTAACTTTGCAAGAGATCTACAGGCATGTACAATCCAGTGTTCCTTATGAACA 1268
 QY 1453 TCGCCCAATAGTATCAAAACGATGTAAATTTATCAATTTTACAAATTTGCTGTAGACCG 1512
 Db 1269 TCGCCCAATAGTATCAAAACGATGTAAATTTATCAATTTTACAAATTTGCTGTAGACCG 1328

QY 1513 AGTGGATGCAGAAGATGGACAGATATGATGTTATGTTTATCGGAAACAGATGTTGGACCGT 1572
 Db 1329 AGTGGATGCAGAAGATGGACAGATATGATGTTATGTTTATCGGAAACAGATGTTGGACCGT 1388
 QY 1573 TCTTAAAGTAGTTTCAATTCCTTAAAGGAGACTTGGTATGATTTAGAAAGAGTTCTGCTGA 1632
 Db 1389 TCTTAAAGTAGTTTCAATTCCTTAAAGGAGACTTGGTATGATTTAGAAAGAGTTCTGCTGA 1448
 QY 1633 AGAATGAACAGTTTTCGGGAAACCGACTGCTATTTTCAAGCAATGGAGCTTTTCCACTAAGCA 1692
 Db 1449 AGAATGAACAGTTTTCGGGAAACCGACTGCTATTTTCAAGCAATGGAGCTTTTCCACTAAGCA 1508
 QY 1693 GAAACAACTATATTTGGTTCAACGGCTGGGGTGCACAGCTCCCTTTTACACGGTGTGA 1752
 Db 1509 GAAACAACTATATTTGGTTCAACGGCTGGGGTGCACAGCTCCCTTTTACACGGTGTGA 1568
 QY 1753 TATTTACGGGAAAGCGTGTGCTGAGTTTCCCTCCCGCCGAGACCTTACTGTGCTTGGGA 1812
 Db 1569 TATTTACGGGAAAGCGTGTGCTGAGTTTCCCTCCCGCCGAGACCTTACTGTGCTTGGGA 1628
 QY 1813 TGGTTCTGCTATGTTCTGCTATTTTCCCACTGCAAGAGACCGCACAGACGACAGATAT 1872
 Db 1629 TGGTTCTGCTATGTTCTGCTATTTTCCCACTGCAAGAGACCGCACAGACGACAGATAT 1688
 QY 1873 AAGAAATGAGACCCCACTGACTGACTGTTTCAAGCTTACACCATGATATACCATGGCCA 1932
 Db 1689 AAGAAATGAGACCCCACTGACTGACTGTTTCAAGCTTACACCATGATATACCATGGCCA 1748
 QY 1933 CAGCCCTGAAGAGAGATCATCTATGTTGTAGAGATAGTAGACATTTTGGATGCGAG 1992
 Db 1749 CAGCCCTGAAGAGAGATCATCTATGTTGTAGAGATAGTAGACATTTTGGATGCGAG 1808
 QY 1993 TCCGAAGTCGACAGAGCGCTGCTTATTTGGCAATTTCCAGAGCGGAAATGAAGAGCGAAA 2052
 Db 1809 TCCGAAGTCGACAGAGCGCTGCTTATTTGGCAATTTCCAGAGCGGAAATGAAGAGCGAAA 1868
 QY 2053 AGAAGATGACAGTGGATGATCATATCATCAGGACAGATCAAGGCCCTTCTCTACGTAG 2112
 Db 1869 AGAAGATGACAGTGGATGATCATATCATCAGGACAGATCAAGGCCCTTCTCTACGTAG 1928
 QY 2113 TCTACAACAGAGAGGATTCAGGCAATTTCTCTGCCATCGGTGGACATGGTTCATACA 2172
 Db 1929 TCTACAACAGAGAGGATTCAGGCAATTTCTCTGCCATCGGTGGACATGGTTCATACA 1988
 QY 2173 AACTCTTCTTAAAGTAAACCTCGAAAGTCATTGACACAGAGCATTTGGAGAACTTCTTCA 2232
 Db 1989 AACTCTTCTTAAAGTAAACCTCGAAAGTCATTGACACAGAGCATTTGGAGAACTTCTTCA 2048
 QY 2233 TAAAGATGATGATGGAGATGGCTCTAAGACCAAGAAATGTCCAAATGACATGACACCTAG 2292
 Db 2049 TAAAGATGATGATGGAGATGGCTCTAAGACCAAGAAATGTCCAAATGACATGACACCTAG 2108
 QY 2293 CCAGAGGTCCTGCTACAGAGACTTTCATGACGCTCATCAACCAACCCCAATCTCAACACGAT 2352
 Db 2109 CCAGAGGTCCTGCTACAGAGACTTTCATGACGCTCATCAACCAACCCCAATCTCAACACGAT 2168
 QY 2353 GGATGAGTTCTGTGAACAAAGTTTGGAAAGGGAACCGAAACAAACGTCGGCAAGGCCAGG 2412
 Db 2169 GGATGAGTTCTGTGAACAAAGTTTGGAAAGGGAACCGAAACAAACGTCGGCAAGGCCAGG 2228
 QY 2413 ACATACCCCAAGGACGCTTACAAATGGAACACTTACAGAAATATAGAAAGGTAGAAA 2472
 Db 2229 ACATACCCCAAGGACGCTTACAAATGGAACACTTACAGAAATATAGAAAGGTAGAAA 2288
 QY 2473 CAGGAGGACCCACGAATTTGAGAGGCGCACCCAGGAGTGTCTGAGCTGATTTACCTCTAGA 2532
 Db 2289 CAGGAGGACCCACGAATTTGAGAGGCGCACCCAGGAGTGTCTGAGCTGATTTACCTCTAGA 2348
 QY 2533 AACCTCAAAACAGTAGAAGACTTGCCTAGACAAATTAACCTGGAAAAACAAATGCAATATACAT 2592
 Db 2349 AACCTCAAAACAGTAGAAGACTTGCCTAGACAAATTAACCTGGAAAAACAAATGCAATATACAT 2408
 QY 2593 GAACTTTTTTTCATGCTATTTATGCTGATGTTTACAAATGGTGGGAAATTCAGCTGAGTTCCA 2652

```

Db 2409 GAACTTTTTCATGCGATATGCGATGTTTACAAATGCGGAAATTCAGGTGATTC 2468
Qy 2653 CCAATTATAAATAATCATCAGTAACCTTTCCATAGGCTTTT 2700
Db 2469 CCAATTATAAATAATCATCAGTAACCTTTCCATAGGCTTTT 2516

RESULT 4
US-10-262-538-9
; Sequence 9, Application US/10262538
; Publication No. US20030113324A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo et al
; TITLE OF INVENTION: NEUROFILIN/VEGF-C/VEGFR-3 MATERIALS AND METHODS
; FILE REFERENCE: 28967/37564
; CURRENT APPLICATION NUMBER: US/10/262,538
; CURRENT FILING DATE: 2002-09-30
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 2530
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (16)..(2331)
US-10-262-538-9

Query Match 92.6%; Score 2508; DB 15; Length 2530;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2508; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 193 CTGAGCATGGCTGGTTAACTAGGATGTCGTTCTTTCTGGGAGTATTACTTACAGC 68
Db 9 CTGAGCATGGCTGGTTAACTAGGATGTCGTTCTTTCTGGGAGTATTACTTACAGC 68

Qy 253 AAGACCAACTATCAGATGGGAGAGCAATGTCGAGGCTCAATATCCTACAAAGA 312
Db 69 AAGACCAACTATCAGATGGGAGAGCAATGTCGAGGCTCAATATCCTACAAAGA 312

Qy 313 AATGTTGAATCCAAATGTGATCCTTTCAATGGCTTGGCCAAAGCTCCAGTTATCA 372
Db 129 AATGTTGAATCCAAATGTGATCCTTTCAATGGCTTGGCCAAAGCTCCAGTTATCA 372

Qy 373 TACCTTCCTTTGGATGAGGACGAGTGTGCTGATGTTGGAGCAAGATCAGATAT 432
Db 189 TACCTTCCTTTGGATGAGGACGAGTGTGCTGATGTTGGAGCAAGATCAGATAT 432

Qy 433 TTCATTGACCTGGTTAATATCAAGGATTTTCAAGATTTGTGCGCCAGTATCTTACAC 492
Db 249 TTCATTGACCTGGTTAATATCAAGGATTTTCAAGATTTGTGCGCCAGTATCTTACAC 492

Qy 493 CAGAGAGCATGATCCAGTGGCTGGAGAGCATCTCAGAGATGCTCAATTTTCAAT 552
Db 309 CAGAGAGCATGATCCAGTGGCTGGAGAGCATCTCAGAGATGCTCAATTTTCAAT 552

Qy 553 CAAGGTACTTAAGGCATATATCAGATCTCTGTCGCTGTGGAACCGGGGCTTTTCA 612
Db 369 CAAGGTACTTAAGGCATATATCAGATCTCTGTCGCTGTGGAACCGGGGCTTTTCA 612

Qy 613 TCCAAATTTGACCTACATTTGAATTTGACATCTCTGAGGAGCAATATTTTAAAGTGA 672
Db 429 TCCAAATTTGACCTACATTTGAATTTGACATCTCTGAGGAGCAATATTTTAAAGTGA 672

Qy 673 GAATCACAATTTGAAAACCGCCCTGGGAGAGTCCAATATGACCCCTAAGCTGTGACAGC 732
Db 489 GAATCACAATTTGAAAACCGCCCTGGGAGAGTCCAATATGACCCCTAAGCTGTGACAGC 732

Qy 733 ATCCCTTTTAAATAGATGAGATATATCTCTGGAATCTGCACTGATTTTATGGGGGAGA 792
Db 549 ATCCCTTTTAAATAGATGAGATATATCTCTGGAATCTGCACTGATTTTATGGGGGAGA 792

```

```

Qy 793 CTTTGTCTATCTTCCGAACTCTTGGGACCAACCACTTGGGAGAGCAGCAGCATGATTC 852
Db 609 CTTTGTCTATCTTCCGAACTCTTGGGACCAACCACTTGGGAGAGCAGCAGCATGATTC 852

Qy 853 CAGGTGGCTCAATGATCCAAAGTTCATTAGTGGCCCACTCATCTCAGAGAGTGACAAATCC 912
Db 669 CAGGTGGCTCAATGATCCAAAGTTCATTAGTGGCCCACTCATCTCAGAGAGTGACAAATCC 912

Qy 913 TGAAGATGACAAAGTATATCTTTTCTTCCGTAATAATGCAATAGATGGGAGCACTCTGG 972
Db 729 TGAAGATGACAAAGTATATCTTTTCTTCCGTAATAATGCAATAGATGGGAGCACTCTGG 972

Qy 973 AAAAGCTACTCAGCTAGATAGTGTGATGATGATGATGATGATGATGATGATGATGATG 1032
Db 789 AAAAGCTACTCAGCTAGATAGTGTGATGATGATGATGATGATGATGATGATGATGATG 1032

Qy 1033 TCTGGTGAATAAATGAGCAACATTTCTTCAAAAGTCTGCTGATTTGCTCAGTGCAGGTC 1092
Db 849 TCTGGTGAATAAATGAGCAACATTTCTTCAAAAGTCTGCTGATTTGCTCAGTGCAGGTC 1092

Qy 1093 AATGCGCATTCAGACTCATTTTGTGATGATGATGATGATGATGATGATGATGATGATGATG 1152
Db 909 AATGCGCATTCAGACTCATTTTGTGATGATGATGATGATGATGATGATGATGATGATGATG 1152

Qy 1153 TCCTAAATAATCCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1212
Db 969 TCCTAAATAATCCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1212

Qy 1213 AGCCGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1272
Db 1029 AGCCGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1272

Qy 1273 CAGGATGAGCCCAACTATCAATGAGTGTGATGATGATGATGATGATGATGATGATGATG 1332
Db 1089 CAGGATGAGCCCAACTATCAATGAGTGTGATGATGATGATGATGATGATGATGATGATGATG 1332

Qy 1333 AGGAACCTGTCAGAGCAAAACATTTGCTGTTGATGATGATGATGATGATGATGATGATGATG 1392
Db 1149 AGGAACCTGTCAGAGCAAAACATTTGCTGTTGATGATGATGATGATGATGATGATGATGATG 1392

Qy 1393 TGTATTAACTTTGCAAGAGTCAATCCAGCTATGATGATGATGATGATGATGATGATGATGATG 1452
Db 1209 TGTATTAACTTTGCAAGAGTCAATCCAGCTATGATGATGATGATGATGATGATGATGATGATG 1452

Qy 1453 TCGCCCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1512
Db 1269 TCGCCCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1512

Qy 1513 AGTGATGCAAGAGATGAGCAGTATGATGATGATGATGATGATGATGATGATGATGATGATG 1572
Db 1329 AGTGATGCAAGAGATGAGCAGTATGATGATGATGATGATGATGATGATGATGATGATGATG 1572

Qy 1573 TCTTAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1632
Db 1389 TCTTAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1632

Qy 1633 AGAAATGACAGTATTTTGGGAAACCGACTCTATTTTTCAGCAATGAGAGCTTTTCCACTAAGCA 1692
Db 1449 AGAAATGACAGTATTTTGGGAAACCGACTCTATTTTTCAGCAATGAGAGCTTTTCCACTAAGCA 1692

Qy 1593 GCAACAATATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1752
Db 1509 GCAACAATATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1752

Qy 1753 TATTTACGGGAAAGCGTGTGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1812
Db 1569 TATTTACGGGAAAGCGTGTGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1812

Qy 1813 TGTCTTCGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1872
Db 1629 TGTCTTCGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1872

Qy 1873 AAGAAATGAGAGCCCACTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1932

```

Db 1689 AAGAAATGAGACCCACTGACTCACTGTTTCAGACTTACACCATGATATCAACCATGAGCA 1748
QY 1933 CAGCCCTGAAGAGAGAAATCACTATGTTGTTAGAGAAATAGTAGACATTTTGGATGAG 1992
Db 1749 CAGCCCTGAAGAGAGAAATCACTATGTTGTTAGAGAAATAGTAGACATTTTGGATGAG 1808
QY 1993 TCCGAAGTCGAGAGAGCGCTGCTATTTGCAATTCAGAGGCGAAATGAAGAGCGAAA 2052
Db 1809 TCCGAAGTCGAGAGAGCGCTGCTATTTGCAATTCAGAGGCGAAATGAAGAGCGAAA 1868
QY 2053 AGAAGAGATCAGAGTGGATGATCATATCATCAGACAGATCAAGGCGCTTCTGCTACCTAG 2112
Db 1869 AGAAGAGATCAGAGTGGATGATCATATCATCAGACAGATCAAGGCGCTTCTGCTACCTAG 1928
QY 2113 TCTCAACAGAGAGATTCAGGCAATTAACCTCTGCGCATGCGGTGGAAATGAGGTTTCATACA 2172
Db 1929 TCTCAACAGAGAGATTCAGGCAATTAACCTCTGCGCATGCGGTGGAAATGAGGTTTCATACA 1988
QY 2173 AACTCTTCTTAAGGTAAACCTGGAAGTCAATTCAGACAGATTTGGAAGAACTTCTTCA 2232
Db 1989 AACTCTTCTTAAGGTAAACCTGGAAGTCAATTCAGACAGATTTGGAAGAACTTCTTCA 2048
QY 2233 TAAAGATCATGATGAGATGCTCTTAAGACCAAGAAATGCCAATAGCATGACACCTAG 2292
Db 2049 TAAAGATCATGATGAGATGCTCTTAAGACCAAGAAATGCCAATAGCATGACACCTAG 2108
QY 2293 CCAGAGGTCGTTACAGAGACTTCATGACGCTCATCAACACCCCAATCTCAACAGAT 2352
Db 2109 CCAGAGGTCGTTACAGAGACTTCATGACGCTCATCAACACCCCAATCTCAACAGAT 2168
QY 2353 GGATGAGTCTGTGAACAAGTTTGGAAAGGACCGAAACAAAGTGGCAAGGCCAGG 2412
Db 2169 GGATGAGTCTGTGAACAAGTTTGGAAAGGACCGAAACAAAGTGGCAAGGCCAGG 2228
QY 2413 ACATACCCAGGAAACAGTAAACAAATGGAAGCACTTACAGAAATTAAGAAAGTAGAAA 2472
Db 2229 ACATACCCAGGAAACAGTAAACAAATGGAAGCACTTACAGAAATTAAGAAAGTAGAAA 2288
QY 2473 CAGAGGACCCAGAAATTTGAGAGGACCCAGAGTGTCTGAGCTGCATTAACCTCTAGA 2532
Db 2289 CAGAGGACCCAGAAATTTGAGAGGACCCAGAGTGTCTGAGCTGCATTAACCTCTAGA 2348
QY 2533 AACCTCAAAACAGTAGAACTTGTCTAGACAAATTAACCTGGAACCAATTAACATATACAT 2592
Db 2349 AACCTCAAAACAGTAGAACTTGTCTAGACAAATTAACCTGGAACCAATTAACATATACAT 2408
QY 2593 GAACCTTTTTCATGCAATATGAGATGTTTACAAATGAGTGGGAAATTCAGCTGAGTTCCA 2652
Db 2409 GAACCTTTTTCATGCAATATGAGATGTTTACAAATGAGTGGGAAATTCAGCTGAGTTCCA 2468
QY 2653 CCAATTATAAATTAATCCATGAGTAACTTTTCCTAATAGGCTTTT 2700
Db 2469 CCAATTATAAATTAATCCATGAGTAACTTTTCCTAATAGGCTTTT 2516

RESULT 5

US-10-067-632-53
; Sequence 53, Application US/10067632
; Publication No. US20030166849A1
; GENERAL INFORMATION:

APPLICANT: Goodman, Corey S.
Kolodkin, Alex L.
Matthes, David
Bentley, David R.
O'Connor, Timothy

TITLE OF INVENTION: The Semaphorin Gene Family

NUMBER OF SEQUENCES: 100

CORRESPONDENCE ADDRESS:

STREET: 268 Bush Street, Suite 3200
CITY: San Francisco
STATE: CA

COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICANT NUMBER: US/10/067,632
FILING DATE: 04-Feb-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/060,610
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/835,268
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A.
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: B94-002-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 2601 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cdna
FEATURE:
NAME/KEY: CDS
LOCATION: 16..2331
SEQUENCE DESCRIPTION: SEQ ID NO: 53:
US-10-067-632-53

Query Match 92.6%; Score 2508; DB 15; Length 2601;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2508; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 193 CTGAGCATGGCTGTTAACTAGGATGTCGTCTTTCTGGGAGTATTACTTACAGC 252

Db 9 CTGAGCATGGCTGTTAACTAGGATGTCGTCTTTCTGGGAGTATTACTTACAGC 68

QY 253 AAGAGCAAACTATCAGATGGGAAGAACAAATGTCAGAGCTGAATATCTTACAAGA 312

Db 69 AAGAGCAAACTATCAGATGGGAAGAACAAATGTCAGAGCTGAATATCTTACAAGA 128

QY 313 AATGTTGGAATCCAACTATGTCATCACTTTCAATGGCTTGGCCACAGCTCCAGTTATCA 372

Db 129 AATGTTGGAATCCAACTATGTCATCACTTTCAATGGCTTGGCCACAGCTCCAGTTATCA 188

QY 373 TACCTTCCTTTTGGATGAGGAACGGAGTAGGCTGTATGTTGGAGCAAGGATCAATATT 432

Db 189 TACCTTCCTTTTGGATGAGGAACGGAGTAGGCTGTATGTTGGAGCAAGGATCAATATT 248

QY 433 TTTCAATTCGACCTGGTTAATATCAAGGATTTTCAAAAGATTTGTCGCCAGTATCTTACAC 492

Db 249 TTTCAATTCGACCTGGTTAATATCAAGGATTTTCAAAAGATTTGTCGCCAGTATCTTACAC 308

QY 493 CAGAAGAGATGAATCAAGTGGGCTGGAAAGACATCTCTGAAAGAAATGTGTAATTTTCA 552

Db 309 CAGAAGAGATGAATCAAGTGGGCTGGAAAGACATCTCTGAAAGAAATGTGTAATTTTCA 368

QY 553 CAAGGTACTTAAGGCATATATCAAGCTCACTTTGACGCTGTGGAACGGGGCTTTTCA 612

Db 369 CAAGGTACTTAAGGCATATATCAAGCTCACTTTGACGCTGTGGAACGGGGCTTTTCA 428

QY 613 TCCAATTTGCACTACATTTGAAATTTGGACATCATCTCGAGGACATATTTTAAAGCTGGA 672

Db 429 TCCAATTTGCACTACATTTGAAATTTGGACATCATCTCGAGGACATATTTTAAAGCTGGA 488

Qy	673	GA	CTCA	CA	TTT	TG	AA	AC	CG	CG	TG	GA	AG	GT	CA	TA	TG	AC	CC	T	A	A	G	C	T	G	C	A	C	A	G	C		7332		
Db	489	GA	CT	CA	CA	TTT	TG	AA	AC	CG	CG	TG	GA	AG	GT	CA	TA	TG	AC	CC	T	A	A	G	C	T	G	C	A	C	A	G	C		548	
Qy	733	AT	CC	CT	TTT	TA	A	T	A	G	T	G	G	A	A	T	T	A	CT	T	G	G	A	A	CT	G	C	A	G	T	G	A	T		792	
Db	549	AT	CC	CT	TTT	TA	A	T	A	G	T	G	G	A	A	T	T	A	CT	T	G	G	A	A	CT	G	C	A	G	T	G	A	T		608	
Qy	793	CT	TT	G	C	T	A	T	CT	T	G	G	C	A	C	C	A	C	C	CA	T	C	A	A	T	C	A	G	A	C	A	G	A		852	
Db	609	CT	TT	G	C	T	A	T	CT	T	G	G	C	A	C	C	A	C	C	CA	T	C	A	A	T	C	A	G	A	C	A	G	A		668	
Qy	853	C	A	G	T	G	C	T	CA	A	T	G	A	T	T	CA	A	A	G	T	T	C	A	A	G	T	T	C	A	A	G	T	G	A		912
Db	669	C	A	G	T	G	C	T	CA	A	T	G	A	T	T	CA	A	A	G	T	T	C	A	A	G	T	T	C	A	A	G	T	G	A		728
Qy	913	T	G	A	G	A	T	G	A	T	G	A	T	G	A	T	G	A	T	G	A	T	G	A	T	G	A	T	G	A	T	G	A		972	
Db	729	T	G	A	G	A	T	G	A	T	G	A	T	G	A	T	G	A	T	G	A	T	G	A	T	G	A	T	G	A	T	G	A		788	
Qy	973	A	A	A	G	C	T	A	C	A	C	T	A	G	A	T	G	A	T	G	A	T	G	A	T	G	A	T	G	A	T	G	A		1032	
Db	789	A	A	A	G	C	T	A	C	A	C	T	A	G	A	T	G	A	T	G	A	T	G	A	T	G	A	T	G	A	T	G	A		848	
Qy	1033	T	C	T	G	G	T	G	A	T	G	A	T	G	A	T	G	A	T	G	A	T	G	A	T	G	A	T	G	A	T	G	A		1092	
Db	849	T	C	T	G	G	T	G	A	T	G	A	T	G	A	T	G	A	T	G	A	T	G	A	T	G	A	T	G	A	T	G	A		908	
Qy	1093	A	A	T	G	G	C	A	T	T	G	A	T	G	A	A	C	T	G	C	A	G	A	T	G	A	T	T	C	T	A	A	T		1152	
Db	909	A	A	T	G	G	C	A	T	T	G	A	T	G	A	A	C	T	G	C	A	G	A	T	G	A	T	T	C	T	A	A	T		968	
Qy	1153	T	C	T	A	A	A	T	C	A	G	T	T	A	T	G	A	T	T	A	G	A	T	T	A	G	A	T	T	A	G	A		1212		
Db	969	T	C	T	A	A	A	T	C	A	G	T	T	A	T	G	A	T	T	A	G	A	T	T	A	G	A	T	T	A	G	A		1028		
Qy	1213	A	G	C	G	T	G	T	A	T	G	A	T	G	A	T	G	A	A	G	G	T	G	T	C	T	T	G	G	T	C	A	T		1272	
Db	1029	A	G	C	G	T	G	T	A	T	G	A	T	G	A	T	G	A	A	G	G	T	G	T	C	T	T	G	G	T	C	A	T		1088	
Qy	1273	C	A	G	G	A	T	G	A	C	C	A	A	C	T	A	T	C	A	A	T	C	A	A	T	C	A	A	T	C	A	A		1332		
Db	1089	C</																																		

1569	DB	TAATTTACGGGAACCGTGTGCTGAGTGTTCCTCGCCCGAGACCTTACTGTGCTTTGGGA	1628
1813	QY	TGGTTCTCGCATGTTCTCGCTATTTTCCACTCGAAAGAGACGCAACAGACGAAGAATAT	1872
1629	DB	TGGTTCTCGATGTTCTCGCTATTTTCCACTCGCAAGAGACGCAACAGACGAAGAATAT	1688
1873	QY	AAGAAATGGAGACCCACTGACTACTCTTTTCAGACTTTCACCATGATTAATCACCATGGCCA	1932
1689	DB	AAGAAATGGAGACCCACTGACTACTCTTTTCAGACTTTCACCATGATTAATCACCATGGCCA	1748
1933	QY	CAGCCCTGAACAGAGAAATCATCTATGCTGTAGAGAAATAGTAGACAATTTTGTGAAATGCAG	1992
1749	DB	CAGCCCTGAACAGAGAAATCATCTATGCTGTAGAGAAATAGTAGACAATTTTGTGAAATGCAG	1808
1993	QY	TCCGAAGTCGAGAGACCGCTGGTCTATTATGGCAATTCACAGAGCGGAATGAAGAGCGAAA	2052
1809	DB	TCCGAAGTCGAGAGACCGCTGGTCTATTATGGCAATTCACAGAGCGGAATGAAGAGCGAAA	1868
2053	QY	AGAAAGATCAGAGTGGATGATCATATCATCAGACACAGATCAAGAGCGCTTCTGCTACGTAG	2112
1869	DB	AGAAAGATCAGAGTGGATGATCATATCATCAGACACAGATCAAGAGCGCTTCTGCTACGTAG	1928
2113	QY	TCTACACAGAGGATTCAGGCAATTAACCTCTGCCATCGCGTGGACATGGTTCATACA	2172
1929	DB	TCTACACAGAGGATTCAGGCAATTAACCTCTGCCATCGCGTGGACATGGTTCATACA	1988
2173	QY	AACCTTTCTTAAAGTAACCCCTGGAAGTCATTGACACAGACANTTGGAGAACTTCTTCA	2232
1989	DB	AACCTTTCTTAAAGTAACCCCTGGAAGTCATTGACACAGACANTTGGAGAACTTCTTCA	2048
2233	QY	TAAAGATGATGAGAGATGGCTCTAGACCAAGAATAATGTCCAATGACATGACACTAG	2292
2049	DB	TAAAGATGATGAGAGATGGCTCTAGACCAAGAATAATGTCCAATGACATGACACTAG	2108
2293	QY	CCGAAGGCTCTGTTACAGAGACTTCATGACGCTCATCAACCACCCCAATCTCAACACGAT	2352
2109	DB	CCGAAGGCTCTGTTACAGAGACTTCATGACGCTCATCAACCACCCCAATCTCAACACGAT	2168
2353	QY	GGATGAGTCTGTGTACAAAGTTTGGAAAAGGACCGAATAACACTCTGGCAAGGCGCAG	2412
2169	DB	GGATGAGTCTGTGTACAAAGTTTGGAAAAGGACCGAATAACACTCTGGCAAGGCGCAG	2228
2413	QY	ACATACCCCGAGGAAACAGTAAACAAATCGAAGCACTTACAAGAAAAATAAGAAAGGTAGAAA	2472
2229	DB	ACATACCCCGAGGAAACAGTAAACAAATCGAAGCACTTACAAGAAAAATAAGAAAGGTAGAAA	2288
2473	QY	CAGAGAGACCCAGAAATTTGAGAGGCGACCCAGGAGTGTCTGAGCTGCATTAACCTCTAG	2532
2289	DB	CAGAGAGACCCAGAAATTTGAGAGGCGACCCAGGAGTGTCTGAGCTGCATTAACCTCTAG	2348
2533	QY	AACCTCAAAACAGTAGAAACTTCGCTAGACAATAACTGGAAAAACAAATGCAATATACAT	2592
2349	DB	AACCTCAAAACAGTAGAAACTTCGCTAGACAATAACTGGAAAAACAAATGCAATATACAT	2408
2593	QY	GAACTTTTTCATGGCAATATGAGATGTTTACAATGGTGGGAAATTCAGCTGAGTTCCA	2652
2409	DB	GAACTTTTTCATGGCAATATGAGATGTTTACAATGGTGGGAAATTCAGCTGAGTTCCA	2468
2653	QY	CCAATTATAAATTAATCCATGATGAACCTTCTCTAATAGGCTTTTTTT	2700
2469	DB	CCAATTATAAATTAATCCATGATGAACCTTCTCTAATAGGCTTTTTTT	2516

RESULT 6
US-09-864-761-30992
: Sequence 30999, Application US/09864761
: Patent No. US20020048763A1
: GENERAL INFORMATION:
: APPLICANT: Petri, Sharon G.
: APPLICANT: Rank, David R.
: APPLICANT: Hanzel, David K.
: APPLICANT: Chen, Wensheng


```

; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Smith, Carole L.
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Farger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: COMPONDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C14
; CURRENT APPLICATION NUMBER: US/10/025,380
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 1129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 736
; LENGTH: 354
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 57
; OTHER INFORMATION: n = A,T,C or G
US-10-025-380-736

Query Match 11.2%; Score 303; DB 14; Length 354;
Best Local Similarity 99.7%; Pred. No. 5e-152;
Matches 353; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2098 CCTCTGCTAGTGTCTACAAACAGAGGATTTCAGGCAATTACCTCTGCATCGGTGGA 2157
DB 1 CCTCTGCTAGTGTCTACAAACAGAGGATTTCAGGCAATTACCTCTGCATCGGTGGA 60

QY 2158 ACATGGGTTTACAAACTCTTTAAGGTAACCTGGAAGTCTTACACAGAGCATTT 2217
DB 61 ACATGGGTTTACAAACTCTTTAAGGTAACCTGGAAGTCTTACACAGAGCATTT 120

QY 2218 GGAAGAACTTCTTCATAAAGATGATGGAGTGGCTTAAAGACCAAGAAATGTCCAA 2277
DB 121 GGAAGAACTTCTTCATAAAGATGATGGAGTGGCTTAAAGACCAAGAAATGTCCAA 180

QY 2278 TAGCATGACACCTAGCCAGAGGCTTGTGTACAGAGACTTCATGAGTCTATCAACCC 2337
DB 181 TAGCATGACACCTAGCCAGAGGCTTGTGTACAGAGACTTCATGAGTCTATCAACCC 240

QY 2338 CAATCTCAACAGATGGATGATGTTCTGTGAACAGATTTGGAAAGGACCGAAACCAACG 2397
DB 241 CAATCTCAACAGATGGATGATGTTCTGTGAACAGATTTGGAAAGGACCGAAACCAACG 300

QY 2398 TCGGCAAGGCCAGGACATACCCAGGGAACAGTAACAAATGGAAGCACTTACA 2451
DB 301 TCGGCAAGGCCAGGACATACCCAGGGAACAGTAACAAATGGAAGCACTTACA 354

RESULT 8
US-09-833-263-736
; Sequence 736, Application US/09833263
; Patent No. US20020110547A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Meagher, Madeleine J.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
; FILE REFERENCE: 210121.471C12
; CURRENT APPLICATION NUMBER: US/09/833,263
; CURRENT FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 736
; LENGTH: 354
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(354)
; OTHER INFORMATION: n = A,T,C or G
US-09-833-263-736

```

```

Query Match 11.2%; Score 303; DB 9; Length 354;
Best Local Similarity 99.7%; Pred. No. 5e-152;
Matches 353; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2098 CCTCTGCTAGTGTCTACAAACAGAGGATTTCAGGCAATTACCTCTGCATCGGTGGA 2157
DB 1 CCTCTGCTAGTGTCTACAAACAGAGGATTTCAGGCAATTACCTCTGCATCGGTGGA 60

QY 2158 ACATGGGTTTACAAACTCTTTAAGGTAACCTGGAAGTCTTACACAGAGCATTT 2217
DB 61 ACATGGGTTTACAAACTCTTTAAGGTAACCTGGAAGTCTTACACAGAGCATTT 120

QY 2218 GGAAGAACTTCTTCATAAAGATGATGGAGTGGCTTAAAGACCAAGAAATGTCCAA 2277
DB 121 GGAAGAACTTCTTCATAAAGATGATGGAGTGGCTTAAAGACCAAGAAATGTCCAA 180

QY 2278 TAGCATGACACCTAGCCAGAGGCTTGTGTACAGAGACTTCATGAGTCTATCAACCC 2337
DB 181 TAGCATGACACCTAGCCAGAGGCTTGTGTACAGAGACTTCATGAGTCTATCAACCC 240

QY 2338 CAATCTCAACAGATGGATGATGTTCTGTGAACAGATTTGGAAAGGACCGAAACCAACG 2397
DB 241 CAATCTCAACAGATGGATGATGTTCTGTGAACAGATTTGGAAAGGACCGAAACCAACG 300

QY 2398 TCGGCAAGGCCAGGACATACCCAGGGAACAGTAACAAATGGAAGCACTTACA 2451
DB 301 TCGGCAAGGCCAGGACATACCCAGGGAACAGTAACAAATGGAAGCACTTACA 354

RESULT 9
US-10-025-380-736
; Sequence 736, Application US/10025380
; Publication No. US20020182191A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather

```

```

; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Smith, Carole L.
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Farger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: COMPONDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C14
; CURRENT APPLICATION NUMBER: US/10/025,380
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 1129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 736
; LENGTH: 354
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 57
; OTHER INFORMATION: n = A,T,C or G
US-10-025-380-736

Query Match 11.2%; Score 303; DB 14; Length 354;
Best Local Similarity 99.7%; Pred. No. 5e-152;
Matches 353; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2098 CCTCTGCTAGTGTCTACAAACAGAGGATTTCAGGCAATTACCTCTGCATCGGTGGA 2157
DB 1 CCTCTGCTAGTGTCTACAAACAGAGGATTTCAGGCAATTACCTCTGCATCGGTGGA 60

QY 2158 ACATGGGTTTACAAACTCTTTAAGGTAACCTGGAAGTCTTACACAGAGCATTT 2217
DB 61 ACATGGGTTTACAAACTCTTTAAGGTAACCTGGAAGTCTTACACAGAGCATTT 120

QY 2218 GGAAGAACTTCTTCATAAAGATGATGGAGTGGCTTAAAGACCAAGAAATGTCCAA 2277
DB 121 GGAAGAACTTCTTCATAAAGATGATGGAGTGGCTTAAAGACCAAGAAATGTCCAA 180

QY 2278 TAGCATGACACCTAGCCAGAGGCTTGTGTACAGAGACTTCATGAGTCTATCAACCC 2337
DB 181 TAGCATGACACCTAGCCAGAGGCTTGTGTACAGAGACTTCATGAGTCTATCAACCC 240

QY 2338 CAATCTCAACAGATGGATGATGTTCTGTGAACAGATTTGGAAAGGACCGAAACCAACG 2397
DB 241 CAATCTCAACAGATGGATGATGTTCTGTGAACAGATTTGGAAAGGACCGAAACCAACG 300

QY 2398 TCGGCAAGGCCAGGACATACCCAGGGAACAGTAACAAATGGAAGCACTTACA 2451
DB 301 TCGGCAAGGCCAGGACATACCCAGGGAACAGTAACAAATGGAAGCACTTACA 354

RESULT 10
US-09-864-761-14444
; Sequence 14444, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aomics-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23

```

PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 14444
LENGTH: 496
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC006322.2
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.73
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.55
US-09-864-761-14444

Query Match 10.8%; Score 292; DB 9; Length 496;
Best Local Similarity 100.0%; Pred. No. 4.4e-146;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2058 AGATCAGAGTGATGATCATATCATCAGGACAGATCAAGGCTTCTGCTACGTAGTCTAC 2117
DB 160 AGATCAGAGTGATGATCATATCATCAGGACAGATCAAGGCTTCTGCTACGTAGTCTAC 219
QY 2118 AACAGAGGATTCAGGCAATTAATCTGCGATGGGTTGGAACATGGGTTTCATACAACTC 2177
DB 220 AACAGAGGATTCAGGCAATTAATCTGCGATGGGTTGGAACATGGGTTTCATACAACTC 279
QY 2178 TTCTTAAGGTAACCTCGAGTCTATTCACACAGAGCAATTTGGAAGACTTCTTCATAAAG 2237
DB 280 TTCTTAAGGTAACCTCGAGTCTATTCACACAGAGCAATTTGGAAGACTTCTTCATAAAG 339
QY 2238 ATGATGATGGAGATGGCTCTAAGACCAAGAAATGTCCAATAGCATGACACCTAGCCAGA 2297
DB 340 ATGATGATGGAGATGGCTCTAAGACCAAGAAATGTCCAATAGCATGACACCTAGCCAGA 399
QY 2298 AGGTCTGTACAGAGATTCATGACGCTCATCAACCAACCCCAATCTCAACAC 2349
DB 400 AGGTCTGTACAGAGATTCATGACGCTCATCAACCAACCCCAATCTCAACAC 451

RESULT 11
US-10-029-386-18184/c
Sequence 18184, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: AEMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 18184
LENGTH: 164
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO CHR7.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.59
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.4
OTHER INFORMATION: SWISSPROT HIT: Q14563, EVALUE 4.00e-29
OTHER INFORMATION: EST HUMAN HIT: BF667677.1, EVALUE 9.00e-81
OTHER INFORMATION: NT HIT: gi16162409, EVALUE 1.00e-85
US-10-029-386-18184

Query Match 5.9%; Score 161; DB 15; Length 164;
Best Local Similarity 100.0%; Pred. No. 1.9e-75;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1691 CAGCAACAACATATATTTGGTTCAACGGTGGGTTGCCAGCTCCCTTTACACGGTGT 1750
DB 164 CAGCAACAACATATATTTGGTTCAACGGTGGGTTGCCAGCTCCCTTTACACGGTGT 105
QY 1751 GATATTTACGGGAAGCGTGTCTGAGTGTTCCTCGCCCGAGACCCCTTACTGTGCTTGG 1810
DB 104 GATATTTACGGGAAGCGTGTCTGAGTGTTCCTCGCCCGAGACCCCTTACTGTGCTTGG 45
QY 1811 GATGTTCTGCATGTTCTCGCTATTTTCCCACTGCAAGAG 1851
DB 44 GATGTTCTGCATGTTCTCGCTATTTTCCCACTGCAAGAG 4

RESULT 12
US-10-029-386-4484/c
Sequence 4484, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: AEMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 4484
LENGTH: 591
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO CHR7.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.59
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.4
OTHER INFORMATION: NT HIT: gi16162409, EVALUE 4.00e-85

OTHER INFORMATION: SWISSPROT HIT: Q14563, EVALUE 2.00e-28
OTHER INFORMATION: EST_HUMAN HIT: BF667677.1, EVALUE 4.00e-80
US-10-029-386-4484

Query Match 5.9%; Score 161; DB 15; Length 591;
Best Local Similarity 100.0%; Pred. No. 2.1e-75; Indels 0; Gaps 0;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1691 CAGCAACAACTATATATGTTGTTCAACGGCTGGGGTTCGCCAGTCCCTTTACCGGTGT 1750
DB 311 CAGCAACAACTATATATGTTGTTCAACGGCTGGGGTTCGCCAGTCCCTTTACCGGTGT 252

QY 1751 GATATTACGGGAAGCGTGTGCTGAGTGTGCTCGCCGAGACCTTACTGTCGTGG 1810
DB 251 GATATTACGGGAAGCGTGTGCTGAGTGTGCTCGCCGAGACCTTACTGTCGTGG 192

QY 1811 GATGGTTCCTCATGTTCTCGCTATTTTCCCACTGCAAGAG 1851
DB 191 GATGGTTCCTCATGTTCTCGCTATTTTCCCACTGCAAGAG 151

RESULT 13
US-09-864-761-27943/c
Sequence 27943, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1

SEQ ID NO 27943
LENGTH: 172
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC004848.1
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2
OTHER INFORMATION: NT HIT: G111421514, EVALUE 8.00e-89
OTHER INFORMATION: EST_HUMAN HIT: BF694785.1, EVALUE 2.30e+00
OTHER INFORMATION: SWISSPROT HIT: Q14563, EVALUE 5.00e-25
US-09-864-761-27943

Query Match 5.9%; Score 160; DB 9; Length 172;
Best Local Similarity 100.0%; Pred. No. 6.7e-75; Indels 0; Gaps 0;
Matches 160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 310 AGAAATGTTGGAATCCCAACATGTGATCACTTTCAATGGCTTGCCCAACAGCTCCAGTTA 369
DB 160 AGAAATGTTGGAATCCCAACATGTGATCACTTTCAATGGCTTGCCCAACAGCTCCAGTTA 101

QY 370 TCATACCTTCCTTTTGGATGAGGAACGGAGTAGGCTCTATGTTGGAGCAAGGATCACAT 429
DB 100 TCATACCTTCCTTTTGGATGAGGAACGGAGTAGGCTCTATGTTGGAGCAAGGATCACAT 41

QY 430 ATTTTCATTCGACCTGGTTAATATCAAGGATTTTCAAAG 469
DB 40 ATTTTCATTCGACCTGGTTAATATCAAGGATTTTCAAAG 1

RESULT 14
US-10-029-386-16491
Sequence 16491, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecomica-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 16491
LENGTH: 191
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO CHR7.1
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.5
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.68
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.64
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.7
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.69
OTHER INFORMATION: SWISSPROT HIT: Q14563, EVALUE 3.00e-25
OTHER INFORMATION: NT HIT: G15174672, EVALUE 5.00e-85
US-10-029-386-16491

Query Match 5.9%; Score 160; DB 15; Length 191;
Best Local Similarity 100.0%; Pred. No. 6.7e-75; Indels 0; Gaps 0;
Matches 160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 310 AGAAATGTTGGAATCCCAACATGTGATCACTTTCAATGGCTTGCCCAACAGCTCCAGTTA 369
DB 11 AGAAATGTTGGAATCCCAACATGTGATCACTTTCAATGGCTTGCCCAACAGCTCCAGTTA 70

QY 370 TCATACCTTCCTTTTGGATGAGGAACGGAGTAGGCTCTATGTTGGAGCAAGGATCACAT 429

OTHER INFORMATION: SWISSPROT HIT: Q14563, EVALUE 2.00e-28
OTHER INFORMATION: EST_HUMAN HIT: BF667677.1, EVALUE 4.00e-80
US-10-029-386-4484

Query Match 5.9%; Score 161; DB 15; Length 591;
Best Local Similarity 100.0%; Pred. No. 2.1e-75; Indels 0; Gaps 0;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1691 CAGCAACAACTATATATGTTGTTCAACGGCTGGGGTTCGCCAGTCCCTTTACCGGTGT 1750
DB 311 CAGCAACAACTATATATGTTGTTCAACGGCTGGGGTTCGCCAGTCCCTTTACCGGTGT 252

QY 1751 GATATTACGGGAAGCGTGTGCTGAGTGTGCTCGCCGAGACCTTACTGTCGTGG 1810
DB 251 GATATTACGGGAAGCGTGTGCTGAGTGTGCTCGCCGAGACCTTACTGTCGTGG 192

QY 1811 GATGGTTCCTCATGTTCTCGCTATTTTCCCACTGCAAGAG 1851
DB 191 GATGGTTCCTCATGTTCTCGCTATTTTCCCACTGCAAGAG 151

RESULT 13
US-09-864-761-27943/c
Sequence 27943, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1

Db 71 TCATACCTTCCTTTGGATGAGGAGTAGCTGTATGTTGGAGCAAGGATCACAT 130
QY 430 ATTTTCATTCGACCTGGTTAATATCAAGGATTTTCAAAAAG 469
Db 131 ATTTTCATTCGACCTGGTTAATATCAAGGATTTTCAAAAAG 170

RESULT 15

US-09-864-761-11363/c
; Sequence 11363, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Acomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 11363
; LENGTH: 484
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC004848.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2
US-09-864-761-11363

Query Match 5.9%; Score 160; DB 9; Length 484;
Best Local Similarity 100.0%; Pred. No. 7.3e-75;
Matches 160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 310 AGAAATGTTGGAATCCAAATGTGATCACTTTCAATGCTTGGCCAAAGCTCCAGTTA 369
Db 458 AGAAATGTTGGAATCCAAATGTGATCACTTTCAATGCTTGGCCAAAGCTCCAGTTA 399
QY 370 TCATACCTTCCTTTTGGATGAGGAGGAGTAGCTGTATGTTGGAGCAAGGATCACAT 429
Db 398 TCATACCTTCCTTTTGGATGAGGAGGAGTAGCTGTATGTTGGAGCAAGGATCACAT 339
QY 430 ATTTTCATTCGACCTGGTTAATATCAAGGATTTTCAAAAAG 469
Db 338 ATTTTCATTCGACCTGGTTAATATCAAGGATTTTCAAAAAG 299

Search completed: September 23, 2004, 08:32:07
Job time : 2147 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 23, 2004, 01:33:05 ; Search time 194 Seconds
(without alignments)
7749.288 Million cell updates/sec

Title: US-09-774-490-1

Perfect score: 2709

Sequence: 1 aatcttttatattcatgatg.....aggcttttttttccataacc 2709

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_NA.*

1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/6C_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2508	92.6	2601	1	US-08-121-713D-53
2	2508	92.6	2601	1	US-08-835-268-53
3	2508	92.6	2601	2	US-08-060-622-53
4	2508	92.6	2601	3	US-08-833-391-53
5	2508	92.6	2601	4	US-08-060-610-53
6	2508	92.6	2601	5	PCT-US94-10151A-53
7	1253	46.3	1481	1	US-08-136-922-1
C 8	31	1.1	7160	4	US-08-786-531B-5
C 9	31	1.1	7235	4	US-08-786-531B-6
C 10	22	0.8	7311	4	US-08-685-004-3
C 11	22	0.8	7352	4	US-08-786-531B-4
C 12	22	0.8	7353	4	US-08-786-531B-1
C 13	22	0.8	7885	4	US-08-645-004-4
14	21	0.8	1062	4	US-09-391-741A-23
15	21	0.8	1062	4	US-09-391-741A-33
16	21	0.8	1181	4	US-08-620-312D-33
17	21	0.8	1385	3	US-08-984-288-1
18	21	0.8	1372	4	US-08-620-312D-664
19	21	0.8	1661	2	US-08-815-176-2
20	21	0.8	1661	4	US-09-197-344-2
21	21	0.8	2026	4	US-09-324-455-1
C 22	20	0.7	30	3	US-08-850-961-31
C 23	20	0.7	30	3	US-09-132-541-5
C 24	20	0.7	30	4	US-08-479-776-31
25	20	0.7	840	4	US-09-244-111-5
26	20	0.7	1008	4	US-09-780-641-1
27	20	0.7	1030	4	US-09-833-381-1211

28 20 0.7 1059 4 US-09-391-741A-9 Sequence 9, Appli
29 20 0.7 1168 4 US-09-620-312D-562 Sequence 562, App
30 20 0.7 1279 3 US-08-985-950-5 Sequence 5, Appli
31 20 0.7 1279 4 US-09-546-049-5 Sequence 5, Appli
32 20 0.7 1338 4 US-09-336-536-1 Sequence 1, Appli
33 20 0.7 1503 3 US-08-999-774A-11 Sequence 11, Appli
34 20 0.7 1770 4 US-09-148-545-102 Sequence 102, App
35 20 0.7 1772 4 US-09-482-273-96 Sequence 96, Appli
36 20 0.7 1772 4 US-09-148-545-46 Sequence 46, Appli
37 20 0.7 1920 4 US-09-620-312D-7 Sequence 7, Appli
38 20 0.7 2214 4 US-09-489-847-113 Sequence 113, App
39 20 0.7 2225 4 US-09-620-312D-1046 Sequence 1046, Ap
40 20 0.7 2227 4 US-09-489-847-30 Sequence 30, Appli
41 20 0.7 2237 4 US-09-561-763-7 Sequence 7, Appli
42 20 0.7 2287 4 US-09-431-367B-7 Sequence 1, Appli
43 20 0.7 4137 3 US-09-221-235-1 Sequence 1, Appli
44 20 0.7 4137 3 US-09-221-928-1 Sequence 1, Appli
45 20 0.7 4137 3 US-09-221-527-1 Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-121-713D-53
; Sequence 53, Application US/08121713D
; Patent No. 5639856
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey S.
; APPLICANT: Kolodkin, Alex L.
; APPLICANT: Matthes, David
; APPLICANT: Bentley, David R.
; APPLICANT: O'Connor, Timothy
; TITLE OF INVENTION: The Semaphorin Gene Family
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 Bush Street, Suite 3200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/121,713D
; FILING DATE: 13-SEP-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B94-002-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)343-4341
; TELEFAX: (415) 343-4342
; TELEX:
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2601 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 16..2331
; US-08-121-713D-53

Query Match 92.6%; Score 2508; DB 1; Length 2601;
Best Local Similarity 100.0%; Pred. No. 0;

	Matches	2508;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	193	CTGCAGCATGGGCTGGTTAACTAGGATGTCTGTCTTTCTGGGAGTATTACTTACAGC	252							
Db	9	CTGCAGCATGGGCTGGTTAACTAGGATGTCTGTCTTTCTGGGAGTATTACTTACAGC	68							
Qy	253	AGAGCAAACTACAGATGGGAGAGCAATGTGCCAGGCTGAAATATCTCTCAAGA	312							
Db	69	AGAGCAAACTATCAGATGGGAGAGCAATGTGCCAGGCTGAAATATCTCTCAAGA	128							
Qy	313	AATGTTGGAATCCAAATGTGATCACTTTCAATGGCTTGGCCACAGCTCCAGTTATCA	372							
Db	129	AATGTTGGAATCCAAATGTGATCACTTTCAATGGCTTGGCCACAGCTCCAGTTATCA	188							
Qy	373	TACCTTCCTTTTGGATGAGGAACGGAGTAGGCTGTATGTTGGAGCAAGGATCAATATT	432							
Db	189	TACCTTCCTTTTGGATGAGGAACGGAGTAGGCTGTATGTTGGAGCAAGGATCAATATT	248							
Qy	433	TTCAATTCGACCTGTGTTAATATCAAGGATTTTCAAAAGATGTGTGGCCAGTATCTTACAC	490							
Db	249	TTCAATTCGACCTGTGTTAATATCAAGGATTTTCAAAAGATGTGTGGCCAGTATCTTACAC	308							
Qy	493	CAGAAGAGATGAATCAAGTCGGCTGGAAAGACATCTTGAAGAAATGTGCTAAATTCAT	552							
Db	309	CAGAAGAGATGAATCAAGTCGGCTGGAAAGACATCTTGAAGAAATGTGCTAAATTCAT	368							
Qy	553	CAAGGTACTTTAAGGCATATAATCAGATCTCATTTGTACGCTGTGGAAACGGGGGTTTTCA	612							
Db	369	CAAGGTACTTTAAGGCATATAATCAGATCTCATTTGTACGCTGTGGAAACGGGGGTTTTCA	428							
Qy	613	TCCAAATTCACCTACATTTGAAATTTGACATCATCTGAGGCAATATTTTTTAAGCTGGA	672							
Db	429	TCCAAATTCACCTACATTTGAAATTTGACATCATCTGAGGCAATATTTTTTAAGCTGGA	488							
Qy	673	GAACTCACATTTTGAAGCGCCGTGGGAAGAGTCAATATGACCCCTAAGCTGCTGACAGC	732							
Db	489	GAACTCACATTTTGAAGCGCCGTGGGAAGAGTCAATATGACCCCTAAGCTGCTGACAGC	548							
Qy	733	ATCCCTTTTAAATAGATGGAGAAATATACTCTGGAACTGCAAGCTGATTTTATGGGGCCAGA	792							
Db	549	ATCCCTTTTAAATAGATGGAGAAATATACTCTGGAACTGCAAGCTGATTTTATGGGGCCAGA	608							
Qy	793	CTTTGCTATCTTCGAACTCTTGGGCACACACCCCAATTCAGGACAGAGAGCATGATTC	852							
Db	609	CTTTGCTATCTTCGAACTCTTGGGCACACACCCCAATTCAGGACAGAGAGCATGATTC	668							
Qy	853	CAGGTGGCTCAATGATCCAAAGTTTCAATTTAGTGCCCACTCATCTCAGAGAGTGCAATCC	912							
Db	669	CAGGTGGCTCAATGATCCAAAGTTTCAATTTAGTGCCCACTCATCTCAGAGAGTGCAATCC	728							
Qy	913	TGAGATGACAAAGTATATCTTTCTCCGTGGAATGCAATAGATGAGAGCAACTCTGG	972							
Db	729	TGAGATGACAAAGTATATCTTTCTCCGTGGAATGCAATAGATGAGAGCAACTCTCTGG	788							
Qy	973	AAAAGCTACTCACGCTAGAATAGGTACAGATATGCAAGAATGACTTTGGAGGGCCACAGAAG	1032							
Db	789	AAAAGCTACTCACGCTAGAATAGGTACAGATATGCAAGAATGACTTTGGAGGGCCACAGAAG	848							
Qy	1033	TCCTGTGATTAATGGACACATCTCTCAAGCTCGTCTGATTTGCTCAGTGCACAGTCC	1092							
Db	849	TCCTGTGATTAATGGACACATCTCTCAAGCTCGTCTGATTTGCTCAGTGCACAGTCC	908							
Qy	1093	AAATGGCATTGACACTCATTTTGATGAACTGCAAGGATGATTTCCCTAATGAATTTAAAGA	1152							
Db	909	AAATGGCATTGACACTCATTTTGATGAACTGCAAGGATGATTTCCCTAATGAATTTAAAGA	968							
Qy	1153	TCTTAAAAATCCAGTTGATATGAGTGTGTTTACGACTCCAGCTAACAATTTTCAAGGGATC	1212							
Db	969	TCTTAAAAATCCAGTTGATATGAGTGTGTTTACGACTCCAGCTAACAATTTTCAAGGGATC	1028							
Qy	1213	AGCCGTGTGATGTATAGCATGATGTATGAGAGGGGTTCCTTGTGTCATATGCCA	1272							
Db	1029	AGCCGTGTGATGTATAGCATGATGTATGAGAGGGGTTCCTTGTGTCATATGCCA	1088							

QY 2353 GGATGAGTCTCTGTAACAAAGTTTGGAAAAGGACCGCAAAACAAACGTCGGCAAGGCCAGG 2412
Db 2169 CGATGAGTCTCTGTAACAAAGTTTGGAAAAGGACCGCAAAACAAACGTCGGCAAGGCCAGG 2228
QY 2413 ACATACCCAGGACGACGTAACAAATGGAAGGACCTACAGAAATAGAAAGGTAGAAA 2472
Db 2229 ACATACCCAGGACGACGTAACAAATGGAAGGACCTACAGAAATAGAAAGGTAGAAA 2288
QY 2473 CAGGAGGACCCACGAATTTGAGAGGCGCACCCAGGAGTGTCTGAGCTGCATTACCTCTAGA 2532
Db 2289 CAGGAGGACCCACGAATTTGAGAGGCGCACCCAGGAGTGTCTGAGCTGCATTACCTCTAGA 2348
QY 2533 AACCTCAACAAAGTGAACCTTGCCTAGACAAATATCTGGAATAACAAATGCAATATACAT 2592
Db 2349 AACCTCAACAAAGTGAACCTTGCCTAGACAAATATCTGGAATAACAAATGCAATATACAT 2408
QY 2593 GAACCTTTTTTCATGCGCATTTATGATGTTTCAATGTTGGAATTCAGCTGAGTTCCA 2652
Db 2409 GAACCTTTTTTCATGCGCATTTATGATGTTTCAATGTTGGAATTCAGCTGAGTTCCA 2458
QY 2653 CCAATATATAATTAATCAATGATGTAACCTTTCTTAATAGGCTTTTTT 2700
Db 2469 CCAATATATAATTAATCAATGATGTAACCTTTCTTAATAGGCTTTTTT 2516

RESULT 2

US-08-835-268-53
; Sequence 53, Application US/08835268
; Patent No. 5807826
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey S.
; APPLICANT: Kolodkin, Alex L.
; APPLICANT: Matthes, David
; APPLICANT: Bentley, David R.
; APPLICANT: O'Connor, Timothy
; TITLE OF INVENTION: The Semaphorin Gene Family
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 Bush Street, Suite 3200
; City: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/835,268
; FILING DATE:
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US/08/121,713
; FILING DATE: 13-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B94-002-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)343-4341
; TELEFAX: (415) 343-4342
; TELEX:
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2601 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS

LOCATION: 16..2331
us-08-835-268-53

Query Match 92.6%; Score 2508; DB 1; Length 2601;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2508; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 193 CTGAGCATGGGCTGGTTAACTAGGATTGCTCTCTTTCTGGGGAGTATTACTTACAGC 252
Db 9 CTGAGCATGGGCTGGTTAACTAGGATTGCTCTCTTTCTGGGGAGTATTACTTACAGC 68
QY 253 AAGAGCAAACTATCAGAAATGGGAAGCAATATGCGCAAGGCTGAAATATATCCACAAAGA 312
Db 69 AAGAGCAAACTATCAGAAATGGGAAGCAATATGCGCAAGGCTGAAATATATCCACAAAGA 128
QY 313 AATCTTGGAAATCAAACTATGATCACTTTCAATGGCTTGGCCAAACAGCTCCAGTTATCA 372
Db 129 AATCTTGGAAATCAAACTATGATCACTTTCAATGGCTTGGCCAAACAGCTCCAGTTATCA 188
QY 373 TACCTTCCCTTTTGGATGAGGAACGGAGTAGGCTGTATGTTGGAGCAAAAGGATCACATATT 432
Db 189 TACCTTCCCTTTTGGATGAGGAACGGAGTAGGCTGTATGTTGGAGCAAAAGGATCACATATT 248
QY 433 TTCATTGCGACCTGGTTAATATCAAGGATTTTCAAAAGATTTGTGCGCCAGTATCTTACAC 492
Db 249 TTCATTGCGACCTGGTTAATATCAAGGATTTTCAAAAGATTTGTGCGCCAGTATCTTACAC 308
QY 493 CAGAAGAGATGAATGCAAGTGGGCTGGAAAGACATCCTGAAAGAAATGTCTAATTTTCAT 552
Db 309 CAGAAGAGATGAATGCAAGTGGGCTGGAAAGACATCCTGAAAGAAATGTCTAATTTTCAT 368
QY 553 CAAGGTACTTAAGGCATATTAATCAGACTCATCTGTAGCGCTGTGGAAACGGGGCTTTTCA 612
Db 369 CAAGGTACTTAAGGCATATTAATCAGACTCATCTGTAGCGCTGTGGAAACGGGGCTTTTCA 428
QY 613 TCCAAATTTGACCTACATATGAAATTTGACATCATCTGAGGACAAATATTTTAAAGCTGGA 672
Db 429 TCCAAATTTGACCTACATATGAAATTTGACATCATCTGAGGACAAATATTTTAAAGCTGGA 488
QY 673 GAACCTACATTTTGAATAACGGCGTGGGAAGAGTCCATATGACCCCTAAGCTGTGACAGC 732
Db 489 GAACCTACATTTTGAATAACGGCGTGGGAAGAGTCCATATGACCCCTAAGCTGTGACAGC 548
QY 733 ATCCCTTTTAATAGATGGGAATTTACTCTGAACTGCAGCTGATTTTATGGGCGAGA 792
Db 549 ATCCCTTTTAATAGATGGGAATTTACTCTGAACTGCAGCTGATTTTATGGGCGAGA 608
QY 793 CTTTGTCTATCTCCGAACCTCTTGGGCACCAACCCCAATCAGGACAGAGCAGCATGATTC 852
Db 609 CTTTGTCTATCTCCGAACCTCTTGGGCACCAACCCCAATCAGGACAGAGCAGCATGATTC 668
QY 853 CAGGTGGCTCAATGATCCAAAGTTTCAATAGTGGCCACCTCATCTCAGAGAGTGACAATCC 912
Db 669 CAGGTGGCTCAATGATCCAAAGTTTCAATAGTGGCCACCTCATCTCAGAGAGTGACAATCC 728
QY 913 TGAAGATGACAAAGTATATCTTTTCTTCGTGAAATCAATAGATGGGAACACATCTGG 972
Db 729 TGAAGATGACAAAGTATATCTTTTCTTCGTGAAATCAATAGATGGGAACACATCTGG 788
QY 973 AAAAGCTACTCAGCTAGAAATAGGTGAGATATGCAAGAATGACTTTTGGAGGGGCACAGAAG 1032
Db 789 AAAAGCTACTCAGCTAGAAATAGGTGAGATATGCAAGAATGACTTTTGGAGGGGCACAGAAG 848
QY 1033 TCTGGTGAATAATGACAAACATTTCTCAAGCTGCTGATTTTGTCTCAGTGCAGGTCC 1092
Db 849 TCTGGTGAATAATGACAAACATTTCTCAAGCTGCTGATTTTGTCTCAGTGCAGGTCC 908
QY 1093 AAATGGCATTGACACTCATTTTGTGAACTGCAGGATGTATTCTCTAATGAATTTAAAGA 1152
Db 909 AAATGGCATTGACACTCATTTTGTGAACTGCAGGATGTATTCTCTAATGAATTTAAAGA 968
QY 1153 TCCTAAAAATCCAGTTGTATATGAGGTGTTTACGACTTCCAGTACATTTTCAAGGATC 1212

STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 16...2331
US-09-060-692-53

Query Match 92.6%; Score 2508; DB 2; Length 2601;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2508; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 193 CTGACGACGCTGGCTGGTTAACTAGGATTTCTCTCTTTCTTCTGGGAGTATTACTTACAGC 252
DB 9 CTGACGACGCTGGCTGGTTAACTAGGATTTCTCTCTTTCTTCTGGGAGTATTACTTACAGC 68
QY 253 AAGAGCAAACTATCAGAAATGGGAAGAACAAATGTGCCAAGGCTGAAATTTATCTCAAGA 312
DB 69 AAGAGCAAACTATCAGAAATGGGAAGAACAAATGTGCCAAGGCTGAAATTTATCTCAAGA 128
QY 313 AATGTTGGAATCCAAACAATGTGATCACTTTCAATGGCTTGGCCCAACAGCTCCAGTTATCA 372
DB 129 AATGTTGGAATCCAAACAATGTGATCACTTTCAATGGCTTGGCCCAACAGCTCCAGTTATCA 188
QY 373 TACCTTCTTTTGGATGAGGAACGAGTAGGCTGTATGTTGGACGAAGGATCACATATT 432
DB 189 TACCTTCTTTTGGATGAGGAACGAGTAGGCTGTATGTTGGACGAAGGATCACATATT 248
QY 433 TTCAATTCGACCTGGTTAAATATCAAGGATTTTCAAGAGATTTGTGGCCAGTATCTTACAC 492
DB 249 TTCAATTCGACCTGGTTAAATATCAAGGATTTTCAAGAGATTTGTGGCCAGTATCTTACAC 308
QY 493 CAGAGAGATCAATGCAAGTGGCTGGGAAGAGATCTGTAAGAGATTTGTGTAATTTTCAAT 552
DB 309 CAGAGAGATCAATGCAAGTGGCTGGGAAGAGATCTGTAAGAGATTTGTGTAATTTTCAAT 368
QY 553 CAAGGTACTTAAGCAATATATCAGACTCACTTGTACGCCCTGTGCAACGGGGCTTTTCA 612
DB 369 CAAGGTACTTAAGCAATATATCAGACTCACTTGTACGCCCTGTGCAACGGGGCTTTTCA 428
QY 613 TCCAAATTTGACCTACATTTGAATTTGACATCATCTTGTAGGACAAATATTTTAAAGCTGGA 672
DB 429 TCCAAATTTGACCTACATTTGAATTTGACATCATCTTGTAGGACAAATATTTTAAAGCTGGA 488
QY 673 GAACTCACATTTTGAAGAGGCTGGGAAGAGTCCATATGACCTTAAGCTGTGACAGC 732
DB 489 GAACTCACATTTTGAAGAGGCTGGGAAGAGTCCATATGACCTTAAGCTGTGACAGC 548
QY 733 ATCCCTTTTATAGATGAGAAATTTATCTCTGGAACCTGCAGCTGATTTTATGGGGGAGA 792
DB 549 ATCCCTTTTATAGATGAGAAATTTATCTCTGGAACCTGCAGCTGATTTTATGGGGGAGA 608
QY 793 CTTTGTCTATCTTCGAACTCTTGGGACACCAACCAATCAGACAGAGCAGCATGATTC 852
DB 609 CTTTGTCTATCTTCGAACTCTTGGGACACCAACCAATCAGACAGAGCAGCATGATTC 668
QY 853 CAGGTGGCTCAATGATCCAAAGTTCAATTAGTGCCCACTCATCTCAGAGAGTGACAAATCC 912
DB 669 CAGGTGGCTCAATGATCCAAAGTTCAATTAGTGCCCACTCATCTCAGAGAGTGACAAATCC 728
QY 913 TGAAGATGACAAAGTATCTTTTCTTCTCGTGAATGCAATGATGGAGAACACTCTGG 972
DB 729 TGAAGATGACAAAGTATCTTTTCTTCTCGTGAATGCAATGATGGAGAACACTCTGG 788
QY 973 AAAAGCTACTCACGCTAGATAGTGTAGATATGCAAGATGATTTGGAGGGGACAGAGAG 1032
DB 789 AAAAGCTACTCACGCTAGATAGTGTAGATATGCAAGATGATTTGGAGGGGACAGAGAG 848
QY 1033 TCTGGTGAATTAAGTGAACAATTTCTCAAGAGTGTGATTTGCTCAGTGCCAGGTCC 1092
DB 849 TCTGGTGAATTAAGTGAACAATTTCTCAAGAGTGTGATTTGCTCAGTGCCAGGTCC 908
QY 1093 AAATGGCATTTGACACTCATTTTGTATGAACTGTCAGGATGATTTCTTAATGAACTTTTCA 1152

DB 909 AAATGGCATTTGACACTCATTTTGTATGAACTGAGGATGATTTCTTAATGAACTTTTAAAGA 968
QY 1153 TCCTAAATATCCAGTTGTATATATGAGATGTTTACGACTTCCAGTAAACATTTTCAAGGATC 1212
DB 969 TCCTAAATATCCAGTTGTATATATGAGATGTTTACGACTTCCAGTAAACATTTTCAAGGATC 1028
QY 1213 AGCGGTGTGTATGTATAGCATGATGTATGAGAGGGTGTCTCTTGGTGCATATGCCCA 1272
DB 1029 AGCGGTGTGTATGTATAGCATGATGTATGAGAGGGTGTCTCTTGGTGCATATGCCCA 1088
QY 1273 CAGGGATGGAACCAACTATCAATGGGTGCTTATCAAGGAAGAGTCCCTATCCAGGCC 1332
DB 1089 CAGGGATGGAACCAACTATCAATGGGTGCTTATCAAGGAAGAGTCCCTATCCAGGCC 1148
QY 1333 AGGAATCTGTCCAGCAAAACATTTGGTGTGTTTGAATCTACAAAGGACCTTCTCTGATGA 1392
DB 1149 AGGAATCTGTCCAGCAAAACATTTGGTGTGTTTGAATCTACAAAGGACCTTCTCTGATGA 1208
QY 1393 TGTATAAACCCTTTGCAAGAGTCAATCCAGGCATGTACAATCCAGTGTCTTCTATGAACAA 1452
DB 1209 TGTATAAACCCTTTGCAAGAGTCAATCCAGGCATGTACAATCCAGTGTCTTCTATGAACAA 1268
QY 1453 TCSCCAATAGTATCAAAACCGATGTAATTTATCAATTTACAAAATTTGTCTGACCG 1512
DB 1269 TCSCCAATAGTATCAAAACCGATGTAATTTATCAATTTACAAAATTTGTCTGACCG 1328
QY 1513 AGTGGATGCAAGAATGGAACAGTATGATGTATGTTTATCGGAACAGATGTTGGGACCGT 1572
DB 1329 AGTGGATGCAAGAATGGAACAGTATGATGTATGTTTATCGGAACAGATGTTGGGACCGT 1388
QY 1573 TCTTAAAGTAGTTTCAATTTCTTAAAGGAGACTTGGTATGATTTTAAAGAGAGTCTCTGTGA 1632
DB 1389 TCTTAAAGTAGTTTCAATTTCTTAAAGGAGACTTGGTATGATTTTAAAGAGAGTCTCTGTGA 1448
QY 1633 AGAATATGACAGTTTTCGGGAACCGACTCTATTTTTCAGCAATGGAAGTTCACACNAAGCA 1692
DB 1449 AGAATATGACAGTTTTCGGGAACCGACTCTATTTTTCAGCAATGGAAGTTCACACNAAGCA 1508
QY 1693 GCAACAACTATATATTTGTTTCAACGGCTGGGGTTCGCCAGCTCCCTTTACACGGTGTGA 1752
DB 1509 GCAACAACTATATATTTGTTTCAACGGCTGGGGTTCGCCAGCTCCCTTTACACGGTGTGA 1568
QY 1753 TATTTACGGGAAGCGTGTGCTGAGTGTGCTTCGCCGAGACCTTACTGTCTTGGGA 1812
DB 1569 TATTTACGGGAAGCGTGTGCTGAGTGTGCTTCGCCGAGACCTTACTGTCTTGGGA 1628
QY 1813 TGGTTCTGATCTTCTCGCTATTTTCCCACTGCAAGAGAGACGCAACAGCAAGATAT 1872
DB 1629 TGGTTCTGATCTTCTCGCTATTTTCCCACTGCAAGAGAGACGCAACAGCAAGATAT 1688
QY 1873 AAGAATGGAAGACCCACTGACTCTGTTTCACTGTTTACACATGATATACCATGGCCA 1932
DB 1689 AAGAATGGAAGACCCACTGACTCTGTTTCACTGTTTACACATGATATACCATGGCCA 1748
QY 1933 CAGCCCTGAAGAGAGAAATCATCTATGTTGTAGAGATAGTAGCAATTTTGGATGAG 1992
DB 1749 CAGCCCTGAAGAGAGAAATCATCTATGTTGTAGAGATAGTAGCAATTTTGGATGAG 1808
QY 1993 TCCGAAGTGCAGAGAGCGCTGGTCTATTGGCAATTTCCAGAGGGGAAATGAAGACCGAAA 2052
DB 1809 TCCGAAGTGCAGAGAGCGCTGGTCTATTGGCAATTTCCAGAGGGGAAATGAAGACCGAAA 1868
QY 2053 AGAAGAGATCAGAGTGGATGATCATATCATCAGACAGATCAAGGCCCTTCTGCTACGTAG 2112
DB 1869 AGAAGAGATCAGAGTGGATGATCATATCATCAGACAGATCAAGGCCCTTCTGCTACGTAG 1928
QY 2113 TCTCAACAGAGAGATTTCAGGCAATTTACTCTGTCATCGGTGGAACATGGTTTCATACA 2172
DB 1929 TCTCAACAGAGAGATTTCAGGCAATTTACTCTGCCATCGCGTGGAACTGGGTTTCATACA 1988
QY 2173 AACTCTTCTTAAAGGTAAACCTTGGAGTGTATGACAGAGCATTTGGAGAACTTCTTCA 2232

1989	Db	AACTCTCTCTTAAGGTAAACCTCGGAAGTCTATGTGACACAGAGCAATTTGGAAAGAACTTCTTCA	2048
2233	Qy	TAAAGATGATGATGGAGATGGCTCTCTAAGAACCAAGAAATGTCCAAATAGCATGACACCTAG	2292
2049	Db	TAAAGATCATGATGGAGATGGCTCTTAGAGACCAAGAAATGTCCAAATAGCATGACACCTAG	2108
2293	Qy	CCAGAAGGTCTGGTACAGAGACTTTCATGACAGTCTCATCAACACCAACCCCAATCTCAACACGAT	2352
2109	Db	CCAGAAGGTCTGGTACAGAGACTTTCATGACAGTCTCATCAACACCAACCCCAATCTCAACACGAT	2168
2353	Qy	GGATGAGTCTCTGTGAAACAGAGTTTGGAAAGGAGGCCGAAACAAAGTGGGCAAGGCCCAGG	2412
2169	Db	GGATGAGTTCTGTGAAACAGTTTGGAAAGGAGGCCGAAACAAAGTGGGCAAGGCCCAGG	2228
2413	Qy	ACATACCCGAGGGAACAGTTAAACAAATGGGAAGCACTTTACAGAAATTAAGAAAGGTAGAAA	2472
2229	Db	ACATACCCGAGGGAACAGTTAAACAAATGGGAAGCACTTTACAGAAATTAAGAAAGGTAGAAA	2288
2473	Qy	CAGGAGGACCCACCAATTTTCAGAGGGGCAACCCAGGAGTGTCTGAGTGCATTAACCTCTAGA	2532
2289	Db	CAGGAGGACCCACCAATTTTCAGAGGGGCAACCCAGGAGTGTCTGAGTGCATTAACCTCTAGA	2348
2533	Qy	AACTCTAAACAGGTAGAAAATTCTCCCTTAGACAAATACTGGAAATAACAAATGCAATATACAT	2592
2349	Db	AACTCTAAACAGGTAGAAAATTCTCCCTTAGACAAATACTGGAAATAACAAATGCAATATACAT	2408
2593	Qy	GAACTTTTTCATGGCAATTATGTGAATGTTTACAATGGTGGGAAATTCAGCTGAGTTCCA	2652
2409	Db	GAACTTTTTCATGGCAATTATGTGAATGTTTACAATGGTGGGAAATTCAGCTGAGTTCCA	2468
2653	Qy	CCAAATTAAATTAATTCATGATGAACCTTCTCCTAATAGGCTTTTCTTTT	2700
2469	Db	CCAAATTAAATTAATTCATGATGAACCTTCTCCTAATAGGCTTTTCTTTT	2516

RESULT 4

US-08-833-391-53
Sequence 53, Application US/08833391
Patent No. 6013781
GENERAL INFORMATION:
APPLICANT: Goodman, Corey S.
APPLICANT: Kolodkin, Alex L.
APPLICANT: Matthes, David R.
APPLICANT: Bentley, David R.
APPLICANT: O'Connor, Timothy
TITLE OF INVENTION: The Semaphorin Gene Family
NUMBER OF SEQUENCES: 190
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 Bush Street, Suite 3200
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,391
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/121,713
FILING DATE: 13-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A.
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: B94-002-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)343-4341
TELEFAX: (415) 343-4342

QY 1033 TCTGTGTAATAAATGGACAACATTCCTCAAAAGTCGTCTGATTTTCTCAGTCCAGGTCC 1092
Db 849 TCTGTGTAATAAATGGACAACATTCCTCAAAAGTCGTCTGATTTTCTCAGTCCAGGTCC 908
QY 1093 AAATGSCATGACACTCAATTTTGTATGAACTGCAGATGTATTCCTAAATGAATTTAAAGA 1152
Db 909 AAATGSCATGACACTCAATTTTGTATGAACTGCAGATGTATTCCTAAATGAATTTAAAGA 968
QY 1153 TCTTAAAAATCAGTGTATATGAGAGTGTATACGACTTCCAGTAAACATTTTCAAGGGATC 1212
Db 969 TCTTAAAAATCAGTGTATATGAGAGTGTATACGACTTCCAGTAAACATTTTCAAGGGATC 1028
QY 1213 AGCCGTGTATGATATAGCATGAGTGTATGAGAGGGTGTCTTGTGTCTATATGCCCCA 1272
Db 1029 AGCCGTGTATGATATAGCATGAGTGTATGAGAGGGTGTCTTGTGTCTATATGCCCCA 1088
QY 1273 CAGGATGAGCCCAACTATCAATGGGTGCTTATCAAGGAAGAGTCCCTTATCCACGGCC 1332
Db 1089 CAGGATGAGCCCAACTATCAATGGGTGCTTATCAAGGAAGAGTCCCTTATCCACGGCC 1148
QY 1333 AGGAATCTGTCCAGCAAAAATTTGGTGTGTTTGAATCTCTACAAAGGACCTTCTCTGATGA 1392
Db 1149 AGGAATCTGTCCAGCAAAAATTTGGTGTGTTTGAATCTCTACAAAGGACCTTCTCTGATGA 1208
QY 1393 TGTTATAACCTTTGCAAGAGTCAATCCAGCCATGTACATCCAGTGTGTTTCTATGAACAA 1452
Db 1209 TGTTATAACCTTTGCAAGAGTCAATCCAGCCATGTACATCCAGTGTGTTTCTATGAACAA 1268
QY 1453 TCGCCCAATAGTATCAAAACGGATGTAAATTTATCAATTTTACAAATTTGCTGTAGACCG 1512
Db 1269 TCGCCCAATAGTATCAAAACGGATGTAAATTTATCAATTTTACAAATTTGCTGTAGACCG 1328
QY 1513 AGTGATGACAGAGATGACAGTATGATTTATGTTTATCGGAACAGATGTTGGGACCGT 1572
Db 1329 AGTGATGACAGAGATGACAGTATGATTTATGTTTATCGGAACAGATGTTGGGACCGT 1388
QY 1573 TCTTAAAGTAGTTTCAATTCCTAAAGAGACTGTGTATGATTTAGAGAGGTTTCTGTGGA 1632
Db 1389 TCTTAAAGTAGTTTCAATTCCTAAAGAGACTGTGTATGATTTAGAGAGGTTTCTGTGGA 1448
QY 1633 AGAATGACAGTCTTTCGGGAACCGACTGTATTTAGCAATGAGCTTTCCTACTAGCA 1692
Db 1449 AGAATGACAGTCTTTCGGGAACCGACTGTATTTAGCAATGAGCTTTCCTACTAGCA 1508
QY 1693 GCAACACTATATATGTTTCAAGCGTGGGTTGCCAGTCCCTTTACACCGGTGGA 1752
Db 1509 GCAACACTATATATGTTTCAAGCGTGGGTTGCCAGTCCCTTTACACCGGTGGA 1568
QY 1753 TATTTACGGGAACCGTGTGCTGAGTGTGCTCGCCGAGACCTTTACTGTGTTGGGA 1812
Db 1569 TATTTACGGGAACCGTGTGCTGAGTGTGCTCGCCGAGACCTTTACTGTGTTGGGA 1628
QY 1813 TGGTCTGCAATGTTCTGCTATTTTCCACTGCAAGAGAGCGCACAGACGACAAGATAT 1872
Db 1629 TGGTCTGCAATGTTCTGCTATTTTCCACTGCAAGAGAGCGCACAGACGACAAGATAT 1688
QY 1873 AAGAAATGGAGACCACTGACTCTGCTGAGTGTGCTCGCCGAGACCTTTACTGTGTTGGGA 1932
Db 1689 AAGAAATGGAGACCACTGACTCTGCTGAGTGTGCTCGCCGAGACCTTTACTGTGTTGGGA 1748
QY 1933 CAGCCCTGAGAGAGATCATCTATGTTGTAGAGATAGTAGACATTTTGGAAATGCGAG 1992
Db 1749 CAGCCCTGAGAGAGATCATCTATGTTGTAGAGATAGTAGACATTTTGGAAATGCGAG 1808
QY 1993 TCCGAAGTCCGAGAGCGGTGGTCTATTTGGCAATTCAGAGCGGAATGAAGAGCGAA 2052
Db 1809 TCCGAAGTCCGAGAGCGGTGGTCTATTTGGCAATTCAGAGCGGAATGAAGAGCGAA 1868
QY 2053 AGAAGATCAGAGTGGATGATCATATCATCAGACAGATCAAGGCTTCTGTACGTAG 2112
Db 1869 AGAAGATCAGAGTGGATGATCATATCATCAGACAGATCAAGGCTTCTGTACGTAG 1928
QY 2113 TCTACACAGAGATTCAGGCAATTACCTCTGCCATGGGTGGAACATGGGTTCTATCA 2172

Db 1929 TCTACACAGAGATTCAGGCAATTACCTCTGCCATGGGTGGAACATGGGTTCTATCA 1988
QY 2173 AACTCTTTTAAAGGTAAACCTCGAAGTCAATGACAGAGCAATTTGGAAGAACTTTCTTCA 2232
Db 1989 AACTCTTTTAAAGGTAAACCTCGAAGTCAATGACAGAGCAATTTGGAAGAACTTTCTTCA 2048
QY 2233 TAAAGATGATGATGGAGATGGCTTAAGACCAAGAAATGCTCAATAGCATGACACCTAG 2292
Db 2049 TAAAGATGATGATGGAGATGGCTTAAGACCAAGAAATGCTCAATAGCATGACACCTAG 2108
QY 2293 CAGAGAGTCTGTTACAGAGACTTCATGAGTCTATCAACCCCAATCTCAACACGAT 2352
Db 2109 CAGAGAGTCTGTTACAGAGACTTCATGAGTCTATCAACCCCAATCTCAACACGAT 2168
QY 2353 GGTAGTCTCTGTAACAAAGTTTGGAAAGGGGACCAAAACACGTCGCGCAAGGCCAGG 2412
Db 2169 GGTAGTCTCTGTAACAAAGTTTGGAAAGGGGACCAAAACACGTCGCGCAAGGCCAGG 2228
QY 2413 ACATACCCAGGGAACAGTAACAAATGGAAGCACCTTACAGAAATAAAGAAAGGTAGAAA 2472
Db 2229 ACATACCCAGGGAACAGTAACAAATGGAAGCACCTTACAGAAATAAAGAAAGGTAGAAA 2288
QY 2473 CAGAGAGCCCAAGAAATTTGAGAGGCCACCCAGGAGTGTCTGAGTGCATTTACTCTAGA 2532
Db 2289 CAGAGAGCCCAAGAAATTTGAGAGGCCACCCAGGAGTGTCTGAGTGCATTTACTCTAGA 2348
QY 2533 AACCTCAAAACAGTAGAAAATTTGCCCTAGACAAATACTGGAATAAATAAGATGCAATATACAT 2592
Db 2349 AACCTCAAAACAGTAGAAAATTTGCCCTAGACAAATACTGGAATAAATAAGATGCAATATACAT 2408
QY 2593 GAACTTTTCTTACGCAATATGAGATGTTTCAATGTTGGGAAATTCAGCTGAGTTCCA 2652
Db 2409 GAACTTTTCTTACGCAATATGAGATGTTTCAATGTTGGGAAATTCAGCTGAGTTCCA 2468
QY 2653 CCAATTAATAATTAATCCATCAGTAACCTTCTCTAATAGGCTTTTCTT 2700
Db 2469 CCAATTAATAATTAATCCATCAGTAACCTTCTCTAATAGGCTTTTCTT 2516

RESULT 5

US-09-060-610-53
; Sequence 53, Application US/09060610
; Patent No. 6344544
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey S.
; APPLICANT: Kolodkin, Alex L.
; APPLICANT: Matthews, David
; APPLICANT: Bentley, David R.
; APPLICANT: O'Connor, Timothy
; TITLE OF INVENTION: The Semaphorin Gene Family
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 Bush Street, Suite 3200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/060.610
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/835,268
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A.

REGISTRATION NUMBER: 36,627
 REFERENCE/DOCKET NUMBER: B94-002-1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 343-4341
 TELEFAX: (415) 343-4342
 TELEX:
 INFORMATION FOR SEQ ID NO: 53:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2601 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 16..2331
 US-09-060-610-53

Query Match 92.6%; Score 2508; DB 4; Length 2601;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2508; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	193	CTGCAGCATGGGCTGGTAACTAGGATTTGCTGCTTTCTGGGGAGTATTACTTACAGC	252
DB	9	CTGCAGCATGGGCTGGTAACTAGGATTTGCTGCTTTCTGGGGAGTATTACTTACAGC	68
QY	253	AAAGAGAACTATCAGATGGGAAGCAACATGTGCCAAGGCTGAATATCTTACAAGA	312
DB	69	AAAGAGAACTATCAGATGGGAAGCAACATGTGCCAAGGCTGAATATCTTACAAGA	128
QY	313	AATGTTGGAATCAACAATGTGATCACTTTTCAATGGCTTGGCCACAGCTCCAGTTATCA	372
DB	129	AATGTTGGAATCAACAATGTGATCACTTTTCAATGGCTTGGCCACAGCTCCAGTTATCA	188
QY	373	TACCTTCCTTTGGATGAGGAACGAGTAGGCTGTATGTTGGAGCAAGGATCACATTT	432
DB	189	TACCTTCCTTTGGATGAGGAACGAGTAGGCTGTATGTTGGAGCAAGGATCACATTT	248
QY	433	TTCAATTCGACCTGGTAAATATCAAGGATTTTCAAAAGATTTGTGGCCAGCTATCTTACAC	492
DB	249	TTCAATTCGACCTGGTAAATATCAAGGATTTTCAAAAGATTTGTGGCCAGCTATCTTACAC	308
QY	493	CAGAGAGATGAATCGAAGTGGCTGGAAAGACATCTGAAAGAAATGTCTAATTTTCAAT	552
DB	309	CAGAGAGATGAATCGAAGTGGCTGGAAAGACATCTGAAAGAAATGTCTAATTTTCAAT	368
QY	553	CAAGGTACTTAAGGCATATAATCAGACTCACTTGTAGCCCTGTGGAAACGGGGCTTTTCA	612
DB	369	CAAGGTACTTAAGGCATATAATCAGACTCACTTGTAGCCCTGTGGAAACGGGGCTTTTCA	428
QY	613	TCCAAATTCACCTACATGAATTTGGACATCATCTTGAGGACAAATATTTTAAAGTGA	672
DB	429	TCCAAATTCACCTACATGAATTTGGACATCATCTTGAGGACAAATATTTTAAAGTGA	488
QY	673	GAACTCACATTTTGAAGACGGCCGTGGGAAGAGTCCATATGACCCTAAGCTGTGACAGC	732
DB	489	GAACTCACATTTTGAAGACGGCCGTGGGAAGAGTCCATATGACCCTAAGCTGTGACAGC	548
QY	733	ATCCCTTTTAAATAGATGAGAAATATATCTCTGGAACCTGCAGCTGATTTTATGGGGGAGA	792
DB	549	ATCCCTTTTAAATAGATGAGAAATATATCTCTGGAACCTGCAGCTGATTTTATGGGGGAGA	608
QY	793	CTTTGCTATCTTCCGAACTCTTTGGGACACCAACCCCAATCAGGACAGAGCAGCATGATTC	852
DB	609	CTTTGCTATCTTCCGAACTCTTTGGGACACCAACCCCAATCAGGACAGAGCAGCATGATTC	668
QY	853	CAGGTGGCTCAATGATCCAAAGTTCATTTAGTGGCCCACTCATCTCAGAGAGTCAATCC	912
DB	669	CAGGTGGCTCAATGATCCAAAGTTCATTTAGTGGCCCACTCATCTCAGAGAGTCAATCC	728
QY	913	TGAAGATGACAAAGTATATCTTTTCTTCCGTGAAAAATGCAATAGATGAGAACTCTGG	972
DB	729	TGAAGATGACAAAGTATATCTTTTCTTCCGTGAAAAATGCAATAGATGAGAACTCTGG	788

QY	973	AAAAGCTACTCAGCTAGATAGGTGAGATATGATGAGAAATGACTTTGGAGGCGACAGAG	1032
DB	789	AAAAGCTACTCAGCTAGATAGGTGAGATATGATGAGAAATGACTTTGGAGGCGACAGAG	848
QY	1033	TCTGTTGAATAAATGGACAACATTCCTCAAGCTCTCTGATTTGCTCAGTCCAGGTCC	1092
DB	849	TCTGTTGAATAAATGGACAACATTCCTCAAGCTCTCTGATTTGCTCAGTCCAGGTCC	908
QY	1093	AAATGGCATTCACACTCATTTTGTATGATGAGTGCAGGATGATTCCTAATGAATTTAAAGA	1152
DB	909	AAATGGCATTCACACTCATTTTGTATGATGAGTGCAGGATGATTCCTAATGAATTTAAAGA	968
QY	1153	TCCTAAAAATCCAGTTGTATATGAGAGTGTTCAGACTTCCAGTAAACATTTCAAGGATC	1212
DB	969	TCCTAAAAATCCAGTTGTATATGAGAGTGTTCAGACTTCCAGTAAACATTTCAAGGATC	1028
QY	1213	AGCCGTGTGTATGATAGCATGATGTGAGAGGGTGTTCCTTGGTCCATATGCCCA	1272
DB	1029	AGCCGTGTGTATGATAGCATGATGTGAGAGGGTGTTCCTTGGTCCATATGCCCA	1088
QY	1273	CAGGATGGACCCCAACTATCAATGGGTGCTTATCAAGGAAGAGTCCCTATCCAGGCC	1332
DB	1089	CAGGATGGACCCCAACTATCAATGGGTGCTTATCAAGGAAGAGTCCCTATCCAGGCC	1148
QY	1333	AGGAACCTGTCCAGCAAAACATTTGGTGTGTTGACTCTACAAAGGACCTTCTGATGA	1392
DB	1149	AGGAACCTGTCCAGCAAAACATTTGGTGTGTTGACTCTACAAAGGACCTTCTGATGA	1208
QY	1393	TGTTATAACCTTTGCAAGAACTCATCCAGCCATGTACAAATCCAGTGTTCCTATGAACAA	1452
DB	1209	TGTTATAACCTTTGCAAGAACTCATCCAGCCATGTACAAATCCAGTGTTCCTATGAACAA	1268
QY	1453	TCGCCCAATAGTGTCAAAACGATGTAAATATCAATTTACAAATTTGCTGAGACG	1512
DB	1269	TCGCCCAATAGTGTCAAAACGATGTAAATATCAATTTACAAATTTGCTGAGACG	1328
QY	1513	AGTGGATGCAAGAGATGGACAGTATGATTTATGTTTATCGGAACAGATGTTGGACCGT	1572
DB	1329	AGTGGATGCAAGAGATGGACAGTATGATTTATGTTTATCGGAACAGATGTTGGACCGT	1388
QY	1573	TCCTAAAGTATGTTCAATTCCTAAGAGACTTGGTATGATTTAGAGAGGTTCTGCTGA	1632
DB	1389	TCCTAAAGTATGTTCAATTCCTAAGAGACTTGGTATGATTTAGAGAGGTTCTGCTGA	1448
QY	1633	AGAAATGACAGTGTTCGGGAACCGACTGCTATTTTCCAGCAATGGAGCTTCCACTAAGCA	1692
DB	1449	AGAAATGACAGTGTTCGGGAACCGACTGCTATTTTCCAGCAATGGAGCTTCCACTAAGCA	1508
QY	1693	GCAACACTATATATTTGGTTCACGGCTGGGTGCTCCAGCTCCCTTTACACCGGTGGA	1752
DB	1509	GCAACACTATATATTTGGTTCACGGCTGGGTGCTCCAGCTCCCTTTACACCGGTGGA	1568
QY	1753	TATTTACGGAAGACGCTGCTGAGTGTTCCTTCGCGCCGAGACCTTTACTGTGCTGGGA	1812
DB	1569	TATTTACGGAAGACGCTGCTGAGTGTTCCTTCGCGCCGAGACCTTTACTGTGCTGGGA	1628
QY	1813	TGGTTCCTGCAATGTTCTGCTATTTTCCACTGCAAGAGACGCAAGAGACAGATAT	1872
DB	1629	TGGTTCCTGCAATGTTCTGCTATTTTCCACTGCAAGAGACGCAAGAGACAGATAT	1688
QY	1873	AAGAAATGGAGACCCACTGCTCAGCTTTTACAGACTTACACCATGATTAATTCACATGGCA	1932
DB	1689	AAGAAATGGAGACCCACTGCTCAGCTTTTACAGACTTACACCATGATTAATTCACATGGCA	1748
QY	1933	CAGCCCTGAGAGAGAAATCATCTATGCTGTAGAGAAATAGTACATTTTGGATTCAG	1992
DB	1749	CAGCCCTGAGAGAGAAATCATCTATGCTGTAGAGAAATAGTACATTTTGGATTCAG	1808
QY	1993	TCGGAAGTCCGAGAGCGCTGCTTATTTGGCAATTCAGAGCGGAAATGAAGAGCGAAA	2052
DB	1809	TCGGAAGTCCGAGAGCGCTGCTTATTTGGCAATTCAGAGCGGAAATGAAGAGCGAAA	1868

QY 2053 AGAGAGATCAGAGTGGATGATATATCATCATCAGACAGATCAAGGCTTCTGCTACGTAG 2112
DB 1869 AGAAGAGATCAGAGTGGATGATATATCATCATCAGACAGATCAAGGCTTCTGCTACGTAG 1928
QY 2113 TCTACAAAGAGAGATTCAGGCAATTAACCTCTGCTGCAATCGGTGGAACAATGCGTTTATACA 2172
DB 1929 TCTACAAAGAGAGATTCAGGCAATTAACCTCTGCTGCAATCGGTGGAACAATGCGTTTATACA 1988
QY 2173 AACTCTTCTTAAGGTAACTCTGGAAGTCAATTCATGACACAGAGATTTGGAAGAACTTTCTCA 2232
DB 1989 AACTCTTCTTAAGGTAACTCTGGAAGTCAATTCATGACACAGAGATTTGGAAGAACTTTCTCA 2048
QY 2233 TAAAGATGATGATGAGATGGCTCTTAAGACCAAGAAATGCTCAATAGCATGACACCTAG 2292
DB 2049 TAAAGATGATGATGAGATGGCTCTTAAGACCAAGAAATGCTCAATAGCATGACACCTAG 2108
QY 2293 CCAGAGTCTGTTACAGAGACTTCATGACGCTCATCAACACCCCAATCTCAACAGAT 2352
DB 2109 CCAGAGTCTGTTACAGAGACTTCATGACGCTCATCAACACCCCAATCTCAACAGAT 2168
QY 2353 GGATGAGTCTGTGAACAACTTTGGAAGAGGACCGAAACCAACGCTGGCAAGGCCAGG 2412
DB 2169 GGATGAGTCTGTGAACAACTTTGGAAGAGGACCGAAACCAACGCTGGCAAGGCCAGG 2228
QY 2413 ACATACCCAGGAGACAGTAACTAAATGGAAGCACTTCAAGAAATTAAGAAAGGTAGAAA 2472
DB 2229 ACATACCCAGGAGACAGTAACTAAATGGAAGCACTTCAAGAAATTAAGAAAGGTAGAAA 2288
QY 2473 CAGGAGGACCCAGCAATTTGAGAGGACCCAGGAGTGTCTGAGCTGATTAACCTCTAGA 2532
DB 2289 CAGGAGGACCCAGCAATTTGAGAGGACCCAGGAGTGTCTGAGCTGATTAACCTCTAGA 2348
QY 2533 AACCTCAAAACAAAGTAGAACTTGCCTAGACAACTAACTGGAACCAAACTGGAATGCAATATACAT 2592
DB 2349 AACCTCAAAACAAAGTAGAACTTGCCTAGACAACTAACTGGAATGCAATATACAT 2408
QY 2593 GAACCTTTTTCATGCAATATGAGATGTTTCAATGAGTGGAAATTCAGCTGAGTCCA 2652
DB 2409 GAACCTTTTTCATGCAATATGAGATGTTTCAATGAGTGGAAATTCAGCTGAGTCCA 2468
QY 2653 CCAATTATAATTAATCCATGAGTAACTTTCTTAATAGGCTTTTTT 2700
DB 2469 CCAATTATAATTAATCCATGAGTAACTTTCTTAATAGGCTTTTTT 2516

RESULT 6

PCT-US94-10151A-53

; Sequence 53, Application PC/TUS9410151A

; GENERAL INFORMATION:

; APPLICANT: The Regents of the University of California

; TITLE OF INVENTION: The Semaphorin Gene Family

; NUMBER OF SEQUENCES: 66

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: FLEHR HOEBACH TEST ALBRITTON & HERBERT

; STREET: 4 Embarcadero Center, Suite 3400

; CITY: San Francisco

; STATE: CA

; COUNTRY: USA

; ZIP: 94111-4187

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US94/10151A

; FILING DATE: 13-SEP-1994

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Osman, Richard A.

; REGISTRATION NUMBER: 36,627

; REFERENCE/DOCKET NUMBER: FP-58750-PC/RAO

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299 FHT UR
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2601 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 16..2331
; PCT-US94-10151A-53

Query Match

92.8%; Score 2508; DB 5; Length 2601;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2508; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 193 CTCGACGATGGGCTGTTAACTAGGATTCCTGCTCTTTCTGGGAGTATTACTTACAGC 252
DB 9 CTCGACGATGGGCTGTTAACTAGGATTCCTGCTCTTTCTGGGAGTATTACTTACAGC 68
QY 253 AAGAGCAAACTATCAGATGGGAAGAAACAATGTGCCAAGGCTGAAATATCTCTACAAAG 312
DB 69 AAGAGCAAACTATCAGATGGGAAGAAACAATGTGCCAAGGCTGAAATATCTCTACAAAG 128
QY 313 AATGTTGGATCAACAATGTGATCACTTTCAATGGCTTGGCCACAGCTCCAGTTTATCA 372
DB 129 AATGTTGGATCAACAATGTGATCACTTTCAATGGCTTGGCCACAGCTCCAGTTTATCA 188
QY 373 TACCTTTCCTTTTGGATGAGGAACGGAGTAGGCTGTATGTTGGAGCAAGAGATCACATAT 432
DB 189 TACCTTTCCTTTTGGATGAGGAACGGAGTAGGCTGTATGTTGGAGCAAGAGATCACATAT 248
QY 433 TTCATTCGACCTGGTTTAATATCAAGGATTTTCAAAAGATTTGTGSCCAGTATCTTACAC 492
DB 249 TTCATTCGACCTGGTTTAATATCAAGGATTTTCAAAAGATTTGTGSCCAGTATCTTACAC 308
QY 493 CAGAAGAGATGAATCAAGTGGGCTGGAAGACATCTCTGAAAGATGTCTAAATTTTCA 552
DB 309 CAGAAGAGATGAATCAAGTGGGCTGGAAGACATCTCTGAAAGATGTCTAAATTTTCA 368
QY 553 CAAGGTACTTAAGGCATATAATCAGACTCATCTGTACGCTCTGGAACCGGGGCTTTTCA 612
DB 369 CAAGGTACTTAAGGCATATAATCAGACTCATCTGTACGCTCTGGAACCGGGGCTTTTCA 428
QY 613 TCCAAATTCACCTACATTTGAAATTTGGACATCATCTGAGGACATATTTTAAAGCTGA 672
DB 429 TCCAAATTCACCTACATTTGAAATTTGGACATCATCTGAGGACATATTTTAAAGCTGA 488
QY 673 GAACTCACATTTTGAAGACCGGCTGGGAAGAGTCCATATGACCTTAAGCTGCTGACAGC 732
DB 489 GAACTCACATTTTGAAGACCGGCTGGGAAGAGTCCATATGACCTTAAGCTGCTGACAGC 548
QY 733 ATCCCTTTTAATAGATGGAGATTTACTCTGGAATGAGTATCTGGAATGAGTATTTATGGGCGAGA 792
DB 549 ATCCCTTTTAATAGATGGAGATTTACTCTGGAATGAGTATTTTATGGGCGAGA 608
QY 793 CTTTGTCTATCTTCGGAACCTTTTGGGCAACCAACCAATCAGGACAGACAGCATGATTC 852
DB 609 CTTTGTCTATCTTCGGAACCTTTTGGGCAACCAACCAATCAGGACAGACAGCATGATTC 668
QY 853 CAGGTGGCTCAATGATCCAAAGTTCATTTAGTGGCCACCTCTCTCAGAGAGTGACAAATCC 912
DB 669 CAGGTGGCTCAATGATCCAAAGTTCATTTAGTGGCCACCTCTCTCAGAGAGTGACAAATCC 728
QY 913 TGAAGATGACAAAGTATATCTTTTCTTCGTCGAAATGCAATAGATGGAGACACTCTGG 972
DB 729 TGAAGATGACAAAGTATATCTTTTCTTCGTCGAAATGCAATAGATGGAGACACTCTGG 788
QY 973 AAAAGCTACTCAGCTAGAAATAGGTGAGATATGCAAGATATGCTTTGGAGGCAACAGAG 1032

Db	789	AAAAGTACTCACGCTAGAAATAGGTCAGATATGCAAGAATGACTTTTGGAGGGCCACAGAAAG	848
Qy	1033	TCCTGGTGAATAAATGACAAACATTCCTCAAAGCTCGTCTGATTTGCTCAGTCCAGGTCC	1092
Db	849	TCTGGTCAATAAATGACAAACATTCCTCAAAGCTCGTCTGATTTGCTCAGTCCAGGTCC	908
Qy	1093	AAATGGCAATTGACATCATTTTGGATGAACTGCGAGGATCTATTCCTTAATGAATTTAAAGA	1152
Db	909	AAATGGCAATTGACATCATTTTGGATGAACTGCGAGGATCTATTCCTTAATGAATTTAAAGA	968
Qy	1153	TCCTAAATAATCCAGTTGTATATGAGAGTGTATTACCACTTCCAGTAAACATTTTCAAGGGATC	1212
Db	969	TCCTAAATAATCCAGTTGTATATGAGAGTGTATTACCACTTCCAGTAAACATTTTCAAGGGATC	1028
Qy	1213	AGCCGTGTGATGTATAGCATAGTGAATGAGAGGGTGTTCCTTGGTCCATATGCCCA	1272
Db	1029	AGCCGTGTGATGTATAGCATAGTGAATGAGAGGGTGTTCCTTGGTCCATATGCCCA	1088
Qy	1273	CAGGATGGACCAACTATCAATGGGTGCCTTATCAAGGAAGAGTCCCTTATCCACGGCC	1332
Db	1089	CAGGATGGACCAACTATCAATGGGTGCCTTATCAAGGAAGAGTCCCTTATCCACGGCC	1148
Qy	1333	AGGAACATTGTCCCAGCAAAAACATTTGGTGGTATTGACTCTACAAAGACCTTCTCTGATGA	1392
Db	1149	AGGAACATTGTCCCAGCAAAAACATTTGGTGGTATTGACTCTACAAAGACCTTCTCTGATGA	1208
Qy	1393	TGTTATAACCTTTGCGAGAAAGTCAATCAGGCATGTACAACTCCAGTGTTCCTTATGAACAA	1452
Db	1209	TGTTATAACCTTTGCGAGAAAGTCAATCAGGCATGTACAACTCCAGTGTTCCTTATGAACAA	1268
Qy	1453	TCGCCCAATAGTGATCAAAACGGATGTAAATTTCAATTTTACAAATTTGCTAGACCG	1512
Db	1269	TCGCCCAATAGTGATCAAAACGGATGTAAATTTCAATTTTACAAATTTGCTAGACCG	1328
Qy	1513	AGTGGATGCGAAGATGGACAGTATGATGTATGTATTTATCGGAACAGATGTTGGGACCGT	1572
Db	1329	AGTGGATGCGAAGATGGACAGTATGATGTATGTATTTATCGGAACAGATGTTGGGACCGT	1388
Qy	1573	TCTTTAAGTAGTTTCAATTCCTAAGGAGACTTGGTATGATTTAGAAAGAGGTTCTGTGGA	1632
Db	1389	TCTTTAAGTAGTTTCAATTCCTAAGGAGACTTGGTATGATTTAGAAAGAGGTTCTGTGGA	1448
Qy	1633	AGAAATGACAGTATTTTCCGGAAACCGACTGTATTTTACGCAATGGAGGTTTCCACTAAGCA	1692
Db	1449	AGAAATGACAGTATTTTCCGGAAACCGACTGTATTTTACGCAATGGAGGTTTCCACTAAGCA	1508
Qy	1693	GCAACACTATATATGGTTTCAACGGCTGGGGTTGCCAGCTCCCTTTACACCGGTGTGA	1752
Db	1509	GCAACACTATATATGGTTTCAACGGCTGGGGTTGCCAGCTCCCTTTACACCGGTGTGA	1568
Qy	1753	TATTTTACGGGAAAGCGTGTGCTGAGTGTTCCTCGCCCGAGACCTTTACTGTGCTGGGA	1812
Db	1569	TATTTTACGGGAAAGCGTGTGCTGAGTGTTCCTCGCCCGAGACCTTTACTGTGCTGGGA	1628
Qy	1813	TGGTTCTGCATGTTCTCGCTATTTTCCACTGCAAGAGGCGCACAGACGACAAGATAT	1872
Db	1629	TGGTTCTGCATGTTCTCGCTATTTTCCACTGCAAGAGGCGCACAGACGACAAGATAT	1688
Qy	1873	AAGAAATGCGACCCCACTGACTCTACTGTTTACAGCTTTACCAATGATTAATCAATGSCCA	1932
Db	1689	AAGAAATGCGACCCCACTGACTCTACTGTTTACAGCTTTACCAATGATTAATCAATGSCCA	1748
Qy	1933	CAGCCCTGAAGAGAGATTCATCTATGGTGTAGAGAAATAGTAGCACATTTTGGAAATCGAG	1992
Db	1749	CAGCCCTGAAGAGAGATTCATCTATGGTGTAGAGAAATAGTAGCACATTTTGGAAATCGAG	1808
Qy	1993	TCCGAAGTCGAGAGAGCGCTGGTCTATTGCGCAATTCAGAGGCGAAATGAAGCGGAAA	2052
Db	1809	TCCGAAGTCGAGAGAGCGCTGGTCTATTGCGCAATTCAGAGGCGAAATGAAGCGGAAA	1868
Qy	2053	AGAAGATATCAGATGGGATGATCATATCATCAGGACAGATCAAGGCCCTTCTGCTACGTAG	2112
Db	1869	AGAAGATATCAGATGGGATGATCATATCATCAGGACAGATCAAGGCCCTTCTGCTACGTAG	1928

RESULT 7

US-08-136-922-1
; sequence 1, Application US/08136922
; Patent No. 5416197

GENERAL INFORMATION:

GENERAL INFORMATION:
APPLICANT: Raper, Jonathan A.

APPLICANT: Luo, Yuling

APPLICANT: DUC, DURING
TITLE OF INVENTION: Compositions Which Regulate Neural

TITLE OF INVENTION: COMPOSITIONS WHICH REGULATE REGENERATION AND METHODS OF MAKING AND USING THE SAME

TITLE OF INVENTION: RE-
NUMBER OF INVENTION: 3
NUMBER OF CO-INVENTORS: 2

NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn

ADDRESSEE: No. 5416197ris

STREET: One I

CITY: Philadelphia

CITY: PHILADELPHIA
STATE: PA

STATE: PA
COUNTRY: USA

COUNTRY: USA
STD: 10103

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: I:

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: P

SUB IMAGE: FACILITY RECORD
CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08

APPLICATION NUMBER:
FILING DATE:

FILING DATE: OCTOBER 1968

CLASSIFICATION: 435

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1481 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: both
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 50..1480
US-08-136-922-1

Query Match 46.3%; Score 1253; DB 1; Length 1481;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1303; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 904 TGCAATCCTGAAGATGACAAAGTATATCTTTTCTCCGTGAAATCAATAGATGAGA 963
DB 58 TGCAATCCTGAAGATGACAAAGTATATCTTTTCTCCGTGAAATCAATAGATGAGA 117
QY 964 ACATCTGGAAGACTACTACGCTAGATAGTTCAGATATGCAAGATGACTTTGAGG 1023
DB 118 ACATCTGGAAGACTACTACGCTAGATAGTTCAGATATGCAAGATGACTTTGAGG 177
QY 1024 GCACAGAGTCTGCTGTAATAATGACAAACATTCCTCAAGCTCGTCTGATTTGCTCAGT 1083
DB 178 GCACAGAGTCTGCTGTAATAATGACAAACATTCCTCAAGCTCGTCTGATTTGCTCAGT 237
QY 1084 GCCAGGTCCTGAAGTTCAGTACATCTTTGATGAGTTCAGATGATTCCTAATGAA 1143
DB 238 GCCAGGTCCTGAAGTTCAGTACATCTTTGATGAGTTCAGATGATTCCTAATGAA 297
QY 1144 CTTTAAAGATCCTAAATCAGTTGTATATGAGAGTGTACGACTTCCAGTACATTTT 1203
DB 298 CTTTAAAGATCCTAAATCAGTTGTATATGAGAGTGTACGACTTCCAGTACATTTT 357
QY 1204 CAAGGATPACCGGTGTATGTATAGCATGATGTGAGAGGGTGTTCCTTGTTCC 1263
DB 358 CAAGGATPACCGGTGTATGTATAGCATGATGTGAGAGGGTGTTCCTTGTTCC 417
QY 1264 ATATGCCACAGGATGACCAACTATCAATGGTGGCTTATCAAGAGAGTCCCTA 1323
DB 418 ATATGCCACAGGATGACCAACTATCAATGGTGGCTTATCAAGAGAGTCCCTA 477
QY 1324 TCCAGGCCAGGAACTTGTCCAGCAAAACATTTGGTGGTGTGACTCTACAAAGGACCT 1383
DB 478 TCCAGGCCAGGAACTTGTCCAGCAAAACATTTGGTGGTGTGACTCTACAAAGGACCT 537
QY 1384 TCCTGATGATGTATTAACCTTTGCAAGAGTCTCCAGCCATGTACAAATCCAGTGTTC 1443
DB 538 TCCTGATGATGTATTAACCTTTGCAAGAGTCTCCAGCCATGTACAAATCCAGTGTTC 597
QY 1444 TATGAACATGCCCAATAGTATGATCAAAAGGATGTAATATCAATTTACACAAATGT 1503
DB 598 TATGAACATGCCCAATAGTATGATCAAAAGGATGTAATATCAATTTACACAAATGT 657
QY 1504 CGTAGACCGAGTGGATGAGAGATGAGCAGTATGATTTATCGGAAACAGATGT 1563
DB 658 CGTAGACCGAGTGGATGAGAGATGAGCAGTATGATTTATCGGAAACAGATGT 717
QY 1564 TGGGACCTTCTTAAGTAGTTTCAATTCCTAAGGAGTGTGATGATTTAGAGAGGT 1623
DB 718 TGGGACCTTCTTAAGTAGTTTCAATTCCTAAGGAGTGTGATGATTTAGAGAGGT 777
QY 1624 TCTGCTGGAAGAAATGACAGTTTTCGGGAACCGACTCTATTTTCAAGATGAGCTTTC 1683
DB 778 TCTGCTGGAAGAAATGACAGTTTTCGGGAACCGACTCTATTTTCAAGATGAGCTTTC 837
QY 1684 CACTAAGCAGCAACCACTATATATGTTTCAACGGCTGGGTTCAGCTCCCTTTTACA 1743

DB 838 CACTAAGCAGCAACCACTATATATGTTTCAACGGCTGGGTTCAGCTCCCTTTACA 897
QY 1744 CCGGTGTGATATTTAGCGGAAAGCGTGTGCTGAGTGTTCCTTCGCCGAGACCTTACTG 1803
DB 898 CCGGTGTGATATTTAGCGGAAAGCGTGTGCTGAGTGTTCCTTCGCCGAGACCTTACTG 957
QY 1804 TCGTTGGGATGTTTCTGCAATGTTCTCGCTATTTTCCCACTGCAAAAGACGCAAGAG 1863
DB 958 TCGTTGGGATGTTTCTGCAATGTTCTCGCTATTTTCCCACTGCAAAAGACGCAAGAG 1017
QY 1864 ACAGGATATAAGAAATGGAGCCCACTGACTCCTGTTTCAGACTTACACCATGATAATCA 1923
DB 1018 ACAAGATATAAGAAATGGAGCCCACTGACTCCTGTTTCAGACTTACACCATGATAATCA 1077
QY 1924 CCATGGCCACAGCCCTGAAGACAGAAATCATCTATGTTGTAGAGAAATAGTAGACATTTT 1983
DB 1078 CCATGGCCACAGCCCTGAAGACAGAAATCATCTATGTTGTAGAGAAATAGTAGACATTTT 1137
QY 1984 GGAATGCACTCCGAAGTCCGACAGAGCGTGTCTATTGGCAATTCAGAGCGCAATGA 2043
DB 1138 GGAATGCACTCCGAAGTCCGACAGAGCGTGTCTATTGGCAATTCAGAGCGCAATGA 1197
QY 2044 AGAGCGAAAGAGAGATCAGATGATCATATCATCATGAGACAGATCAAGGCTTCT 2103
DB 1198 AGAGCGAAAGAGAGATCAGATGATCATATCATCATGAGACAGATCAAGGCTTCT 1257
QY 2104 GTTACGTAGTCTACAAAGAGATTCAGGCAATTAACCTTCCCATGCGGTGGAACATGG 2163
DB 1258 GTTACGTAGTCTACAAAGAGATTCAGGCAATTAACCTTCCCATGCGGTGGAACATGG 1317
QY 2164 GTTCATACAACTCTTCTTAAGGTAACTGCAAGTCAATTGACA 2207
DB 1318 GTTCATACAACTCTTCTTAAGGTAACTGCAAGTCAATTGACA 1361

RESULT 8

US-08-786-531B-5/c

; Sequence 5, Application US/08786531B

; Patent No. 6541197

; GENERAL INFORMATION:

; APPLICANT: Link, Charles J.

; APPLICANT: Levy, John P.

; APPLICANT: Wang, Suming

; APPLICANT: Seragina, Tatiana

; TITLE OF INVENTION: Vehicles for Stable Transfer of Green

; TITLE OF INVENTION: Fluorescent Protein Gene and Methods of Use for Same

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Zarley, McKee, Thomte, Voorhees & Sease

; STREET: 801 Grand Suite 3200

; CITY: Des Moines

; STATE: Iowa

; COUNTRY: United States

; ZIP: 50309

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/786,531B

; FILING DATE: 21-JAN-1997

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/010371

; FILING DATE: 22-JAN-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Nebel, Heidi S.

; REGISTRATION NUMBER: 37,719

; REFERENCE/DOCKET NUMBER: hgr1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 515-288-3667

; TELEFAX: 515-288-1338

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 7160 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-786-531B-5

Query Match 1.1%; Score 31; DB 4; Length 7160;
Best Local Similarity 100.0%; Pred. No. 4.3e-05;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATCTTTTATTTATCGATGTTAACAAGCTT 31
DB 4179 AATCTTTTATTTATCGATGTTAACAAGCTT 4149

RESULT 9

US-08-786-531B-6/c
Sequence 6, Application US/08786531B

Patent No. 6541197

GENERAL INFORMATION:

APPLICANT: Link, Charles J.

APPLICANT: Levy, John P.

APPLICANT: Wang, Suming

APPLICANT: Seregina, Tatiana

TITLE OF INVENTION: Vehicles for Stable Transfer of Green

TITLE OF INVENTION: Fluorescent Protein Gene and Methods of Use for Same

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Zarley, McKee, Thome, Voorhees & Sease

STREET: 801 Grand Suite 3200

CITY: Des Moines

STATE: Iowa

COUNTRY: United States

ZIP: 50309

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/786,531B

FILING DATE: 21-JAN-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/010371

FILING DATE: 22-JAN-1996

ATTORNEY/AGENT INFORMATION:

NAME: Nebel, Heidi S.

REGISTRATION NUMBER: 37,719

REFERENCE/DOCKET NUMBER: Hgtri

TELECOMMUNICATION INFORMATION:

TELEPHONE: 515-288-3667

TELEFAX: 515-288-1338

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 7235 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-08-786-531B-6

Query Match 1.1%; Score 31; DB 4; Length 7235;
Best Local Similarity 100.0%; Pred. No. 4.3e-05;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATCTTTTATTTATCGATGTTAACAAGCTT 31
DB 4254 AATCTTTTATTTATCGATGTTAACAAGCTT 4224

RESULT 10

US-09-645-004-3/c

Sequence 3, Application US/09645004

Patent No. 6608238

GENERAL INFORMATION:

APPLICANT: Gavora, Jan S.

APPLICANT: Falconer, Marcia M.

APPLICANT: Nguyen, Thuy H.

APPLICANT: Benkel, Bernhard F.

TITLE OF INVENTION: Trans-Somatics With Gene Transfer Into Mammary Epithelial Cells

FILE REFERENCE: GALA-06402

CURRENT APPLICATION NUMBER: US/09/645,004

CURRENT FILING DATE: 2000-08-24

NUMBER OF SEQ ID NOS: 4

SOFTWARE: Patent in version 3.2

SEQ ID NO 3

LENGTH: 7311

TYPE: DNA

ORGANISM: Artificial

FEATURE:

OTHER INFORMATION: Plasmid pLNNX

US-09-645-004-3

Query Match 0.8%; Score 22; DB 4; Length 7311;

Best Local Similarity 100.0%; Pred. No. 0.97;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATCTTTTATTTATCGATGTT 22
DB 4330 AATCTTTTATTTATCGATGTT 4309

RESULT 11

US-08-786-531B-4/c

Sequence 4, Application US/08786531B

Patent No. 6541197

GENERAL INFORMATION:

APPLICANT: Link, Charles J.

APPLICANT: Levy, John P.

APPLICANT: Wang, Suming

APPLICANT: Seregina, Tatiana

TITLE OF INVENTION: Vehicles for Stable Transfer of Green

TITLE OF INVENTION: Fluorescent Protein Gene and Methods of Use for Same

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Zarley, McKee, Thome, Voorhees & Sease

STREET: 801 Grand Suite 3200

CITY: Des Moines

STATE: Iowa

COUNTRY: United States

ZIP: 50309

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/786,531B

FILING DATE: 21-JAN-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/010371

FILING DATE: 22-JAN-1996

ATTORNEY/AGENT INFORMATION:

NAME: Nebel, Heidi S.

REGISTRATION NUMBER: 37,719

REFERENCE/DOCKET NUMBER: Hgtri

TELECOMMUNICATION INFORMATION:

TELEPHONE: 515-288-3667
TELEFAX: 515-288-1338
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 7352 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-786-531B-4

Query Match 0.8%; Score 22; DB 4; Length 7352;
Best Local Similarity 100.0%; Pred. No. 0.97;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATCTTTTATTTATCGATGTT 22
|||||
DB 4371 AATCTTTTATTTATCGATGTT 4350

RESULT 12

US-08-786-531B-1/c
Sequence 1, Application US/08786531B
Patent No. 6541197
GENERAL INFORMATION:
APPLICANT: Link, Charles J.
APPLICANT: Levy, John P.
APPLICANT: Wang, Suming
APPLICANT: Seragina, Tatiana
TITLE OF INVENTION: Vehicles for Stable Transfer of Green
TITLE OF INVENTION: Fluorescent Protein Gene and Methods of Use for Same
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zarley, McKee, Thonthe, Voorhees & Sease
STREET: 801 Grand Suite 3200
CITY: Des Moines
STATE: Iowa
COUNTRY: United States
ZIP: 50309

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/786.531B
FILING DATE: 21-JAN-1997

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/010371
FILING DATE: 22-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Nebel, Heidi S.
REGISTRATION NUMBER: 37,719
REFERENCE/DOCKET NUMBER: R9c1r
TELECOMMUNICATION INFORMATION:
TELEPHONE: 515-288-3667
TELEFAX: 515-288-1338
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 7353 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: other nucleic acid
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-786-531B-1

Query Match 0.8%; Score 22; DB 4; Length 7353;
Best Local Similarity 100.0%; Pred. No. 0.97;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AATCTTTTATTTATCGATGTT 22
|||||
DB 4372 AATCTTTTATTTATCGATGTT 4351

RESULT 13

US-09-645-004-4/c
Sequence 4, Application US/09645004
Patent No. 6608238
GENERAL INFORMATION:
APPLICANT: Gavora, Jan S.
APPLICANT: Falconer, Marcia M.
APPLICANT: Nguyen, Thuy H.
APPLICANT: Benkel, Bernhard F.
TITLE OF INVENTION: Trans-Somatics With Gene-Transfer Into Mammary Epithelial Cells
FILE REFERENCE: GALA-06402
CURRENT APPLICATION NUMBER: US/09/645,004
CURRENT FILING DATE: 2000-08-24
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patent in version 3.2
SEQ ID NO 4
LENGTH: 7885
TYPE: DNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Plasmid pLNM12X
US-09-645-004-4

Query Match 0.8%; Score 22; DB 4; Length 7885;
Best Local Similarity 100.0%; Pred. No. 0.97;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATCTTTTATTTATCGATGTT 22
|||||
DB 4904 AATCTTTTATTTATCGATGTT 4883

RESULT 14

US-09-391-741A-23
Sequence 23, Application US/09391741A
Patent No. 6555732
GENERAL INFORMATION:
APPLICANT: Duvick, Jonathan P.
APPLICANT: Sharma, Yogesh Kumar
TITLE OF INVENTION: Rac-Like Genes and Methods of Use
FILE REFERENCE: 0866D
CURRENT APPLICATION NUMBER: US/09/391,741A
CURRENT FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: 60/111,919
PRIOR FILING DATE: 1998-12-11
PRIOR APPLICATION NUMBER: 60/100,284
PRIOR FILING DATE: 1998-09-14
PRIOR APPLICATION NUMBER: 09/391,741
PRIOR FILING DATE: 1999-09-08
NUMBER OF SEQ ID NOS: 51
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 23
LENGTH: 1062
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: CDS
LOCATION: (172)...(807)
US-09-391-741A-23

Query Match 0.8%; Score 21; DB 4; Length 1062;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 57 GTCGACCCACGGCTCCGGGAG 77
|||||

Thu Sep 23 08:54:05 2004

Db 3 GTCGACCCACGCGTCCGGGAG 23

RESULT 15

US-09-391-741A-33
 ; Sequence 33, Application US/09391741A
 ; Patent No. 6555732
 ; GENERAL INFORMATION:
 ; APPLICANT: Duwick, Jonathan P.
 ; APPLICANT: Sharma, Yogesh Kumar
 ; TITLE OF INVENTION: Rac-Like Genes and Methods of Use
 ; FILE REFERENCE: 0866D
 ; CURRENT APPLICATION NUMBER: US/09/391,741A
 ; CURRENT FILING DATE: 1999-09-08
 ; PRIOR APPLICATION NUMBER: 60/111,919
 ; PRIOR FILING DATE: 1998-12-11
 ; PRIOR APPLICATION NUMBER: 60/100,284
 ; PRIOR FILING DATE: 1998-09-14
 ; PRIOR APPLICATION NUMBER: 09/391,741
 ; PRIOR FILING DATE: 1999-09-08
 ; NUMBER OF SEQ ID NOS: 51
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 33
 ; LENGTH: 1062
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (172)...(807)
 US-09-391-741A-33

Query Match 0.8%; Score 21; DB 4; Length 1062;
 Best Local Similarity 100.0%; Pred. No. 3;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 57 GTCGACCCACGCGTCCGGGAG 77
 |||||
 Db 3 GTCGACCCACGCGTCCGGGAG 23

Search completed: September 23, 2004, 05:10:25
 Job time : 204 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: September 21, 2004, 19:45:33 ; Search time 303 Seconds
(without alignments)
5742.244 Million cell updates/sec

Title: US-09-774-490-1

Perfect score: 4896

Sequence: 1 aactctttatttcgatg.....aggcttttttcctaataacc 2709

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1342398 seqs, 321133274 residues

Total number of hits satisfying chosen parameters: 2684796

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame_n2p.model -DEV=xl
-Q=/cgn2_1/USPTO.spool_p/US09774490/runat_21092004.144248.2409/app_query.fasta.1.2887
-DB=Published Applications AA -QWMT=fastan -SUFFIX=rapb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCLALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USRR=US09774490 @CGN 1 1 453 @runat_21092004.144248.2409
-NCPU=6 -ICPU=3 -NO MMAP -LARGESQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -2409
-LONGLOG -DEV -TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications AA:

1: /cgn2_6/prodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/prodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/prodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/prodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/prodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/prodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/prodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/prodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/prodata/2/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_6/prodata/2/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/prodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/prodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/prodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/prodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/prodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/prodata/2/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/prodata/2/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/prodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description

ALIGNMENTS

RESULT 1

US-10-097-340-284
; Sequence 284, Application US/10097340
; Publication No. US20030087250A1
; GENERAL INFORMATION:
; APPLICANT: John MONAHAN
; APPLICANT: Marjula GANNAVAPURU
; APPLICANT: Sebastian HOERSCHE
; APPLICANT: Shubhangi KAMATKAR
; APPLICANT: Steve G. KOVATS
; APPLICANT: Rachel E. MEYERS
; APPLICANT: Michael MORRISSEY
; APPLICANT: Peter OLANDT
; APPLICANT: Ami SEN
; APPLICANT: Peter VEIBY
; APPLICANT: Gordon B. MILLS
; APPLICANT: Robert C. BAST, Jr.
; APPLICANT: Karen LU
; APPLICANT: Rosemarie SCHMANDT
; APPLICANT: Xumei ZHAO
; APPLICANT: Karen GLATT
; TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
; TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
; FILE REFERENCE: MRI-030

Sequence 284, App	US-10-097-340-284	771	14
Sequence 10, Appl	US-10-262-538-10	771	14
Sequence 54, Appl	US-10-067-632-54	771	14
Sequence 164, Appl	US-10-247-671-164	771	14
Sequence 3, Appli	US-10-320-769-3	655	14
Sequence 310, App	US-09-946-374-310	777	12
Sequence 348, App	US-10-206-915-348	777	12
Sequence 348, App	US-10-199-670-348	777	12
Sequence 348, App	US-10-201-858-348	777	12
Sequence 348, App	US-10-205-890-348	777	12
Sequence 348, App	US-10-208-024-348	777	12
Sequence 348, App	US-10-201-853-348	777	12
Sequence 348, App	US-10-174-581-348	777	12
Sequence 348, App	US-10-176-483-348	777	12
Sequence 348, App	US-10-176-749-348	777	12
Sequence 348, App	US-10-176-915-348	777	12
Sequence 348, App	US-10-176-915-348	777	12
Sequence 310, App	US-10-006-485A-310	777	12
Sequence 310, App	US-10-013-907A-310	777	12
Sequence 310, App	US-10-015-499A-310	777	12
Sequence 348, App	US-10-176-484-348	777	12
Sequence 348, App	US-10-180-550-348	777	12
Sequence 348, App	US-10-183-014-348	777	12
Sequence 348, App	US-10-187-738-348	777	12
Sequence 348, App	US-10-187-740-348	777	12
Sequence 348, App	US-10-187-883-348	777	12
Sequence 348, App	US-10-194-363-348	777	12
Sequence 348, App	US-10-194-460-348	777	12
Sequence 348, App	US-10-194-463-348	777	12
Sequence 348, App	US-10-194-484-348	777	12
Sequence 348, App	US-10-195-884-348	777	12
Sequence 348, App	US-10-195-896-348	777	12
Sequence 348, App	US-10-196-744-348	777	12
Sequence 348, App	US-10-196-755-348	777	12
Sequence 348, App	US-10-196-757-348	777	12
Sequence 348, App	US-10-197-704-348	777	12
Sequence 348, App	US-10-198-758-348	777	12
Sequence 348, App	US-10-198-766-348	777	12
Sequence 348, App	US-10-199-304-348	777	12
Sequence 348, App	US-10-199-309-348	777	12
Sequence 348, App	US-10-199-313-348	777	12
Sequence 348, App	US-10-199-456-348	777	12
Sequence 348, App	US-10-201-329-348	777	12
Sequence 348, App	US-10-202-412-348	777	12

CURRENT APPLICATION NUMBER: US/10/037,340
 CURRENT FILING DATE: 2002-03-14
 PRIOR APPLICATION NUMBER: 60/276,025
 PRIOR FILING DATE: 2001-03-14
 PRIOR APPLICATION NUMBER: 60/325,149
 PRIOR FILING DATE: 2001-09-26
 PRIOR APPLICATION NUMBER: 60/276,026
 PRIOR FILING DATE: 2001-03-14
 PRIOR APPLICATION NUMBER: 60/324,967
 PRIOR FILING DATE: 2001/09/26
 PRIOR APPLICATION NUMBER: 60/311,732
 PRIOR FILING DATE: 2001-08-10
 PRIOR APPLICATION NUMBER: 60/325,102
 PRIOR FILING DATE: 2001-09-26
 PRIOR APPLICATION NUMBER: 60/323,580
 PRIOR FILING DATE: 2001-09-19
 NUMBER OF SEQ ID NOS: 363
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 284
 LENGTH: 771
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-097-340-284

Alignment Scores:
 Pred. No.: 0 Length: 771
 Score: 4201.00 Matches: 771
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 85.80% Indels: 0
 DB: 14 Gaps: 0

US-09-774-490-1 (1-2709) x US-10-097-340-284 (1-771)

QY	200	ATGGGCTGTTAACTAGGATGCTGCTCTTTCTGGGAGTATTACTACAGCAGACA	259
DB	1	MetGlyTrpLeuThrArgIleValCysLeuPheTrpGlyValLeuLeuThrAlaArgAla	20
QY	260	AACATACAGAAATGGGAAGAACAAATGTCCCAAGCTGAAATATATCTCAAAAGAAATGTTG	319
DB	21	AsnTyrGluAsnGlyLysAsnValProAlaGlyLeuLysLeuSerTyrLysGluMetLeu	40
QY	320	GAATCCAAACATGTGATCATCTTTCAATGCTTGGCCCAACAGCTCAGATATCATACCTTC	379
DB	41	GluSerAsnValIleThrPheAsnGlyLeuAlaAsnSerSerTyrHisThrPhe	60
QY	380	CTTTTGGATGAGCAACGAGTAGGCTGTATGTTGGAGCAAGGATCACATATTTTCATTC	439
DB	61	LeuLeuAspGluGluArgSerArgLeuTyrValGlyAlaLysAspHisIlePheSerPhe	80
QY	440	GACCTGTTAATATCAAGATTTTCAAAAGATGTGTGGCCAGTATCTTACACCAAGA	499
DB	81	AspLeuValAsnIleLysAspPheGlnLysIleValTrpProValSerTyrThrArg	100
QY	500	GATGAATGCAAGTGGCTGGAAGACATCTCTGAAGATGCTAAATTTTCATCAAGTA	559
DB	101	AspGluCysLysTrpAlaGlyLysAspIleLeuLysGluCysAlaAsnPheIleLysVal	120
QY	560	CTTAAGGCATATATATCAGACTCATTGTACGCTGTGGAAACGGGGCTTTTCATCAATT	619
DB	121	LeuLysAlaTyrAsnGlnThrHisLeuTyrAlaCysGlyThrGlyAlaPheHisProIle	140
QY	620	TGCACCTACATTTGAATATGACATCATCTGAGGACATATTTTAAAGTGGAGACTCA	679
DB	141	CysThrTyrIleGluIleGlyHisHisProGluAspAsnIlePheLysLeuGluAsnSer	160
QY	680	CATTTTGAACCGGCTGGGAGAGTCCATATGACCTTAAGCTGTGACAGCATCCCTT	739
DB	161	HisPheGluAsnGlyArgGlyLysSerProTyrAspProLysLeuLeuThrAlaSerLeu	180
QY	740	TTAATGATGGAGAAATATATCTCGAAGTGCAGCTGATTTTATGGGGGAGACTTGTCT	799
DB	181	LeuIleAspGlyLeuTyrSerGlyThrAlaAlaAspPheMetGlyArgAspPheAla	200

QY	800	ATCTTCGGAACCTCTTGGGACACACCAATCAGACAGACAGCATGATTCAGGTGG	859
DB	201	IlePheArgThrLeuGlyHisHisProIleArgThrGluGlnHisAspSerArgTrp	220
QY	860	CTCAATGATCCAAAGTTTCATTAGTCCACCTCATCTCAGAGAGTACAAATCTCTGAAGAT	919
DB	221	LeuAsnAspProLysPheIleSerAlaHisLeuIleSerGluSerAspAsnProGluAsp	240
QY	920	GACAAAGTATATCTTTCTTCGTAAGTGAATGAAATAGATGGAGACACATCTCGAAAAGCT	979
DB	241	AspLysValTyrPhePheArgGluAsnAlaIleAspGlyGluHisSerGlyLysAla	260
QY	980	ACTCAGCTAGATAGTACAGATATGCAAGAATGACTTTGGAGGGCACAAGAAGTCTGTG	1039
DB	261	ThrHisAlaArgIleGlyGlnIleCysLysAsnAspPheGlyGlyHisArgSerLeuVal	280
QY	1040	AATAAATGACAAACATCTCTCAAGCTCTCTGATTTGCTCAGTCCAGGTCCTCAATGGC	1099
DB	281	AsnLysTrpThrThrPheLeuLysAlaArgLeuIleCysSerValProGlyProAsnGly	300
QY	1100	ATTGACACTCATTTTTCATGAACTGCAGGATGATTCCTAATGAACCTTTAAAGATCTTAA	1159
DB	301	IleAspThrHisPheAspGluLeuGlnAspValPheLeuMetAsnPheLysAspProLys	320
QY	1160	AATCCAGTTGTATATGAGTGTTCACACTTCCAGTAAACATTTTCAAGGGATCAGCCGTG	1219
DB	321	AsnProValValTyrGlyValPheThrThrSerSerAsnIlePheLysGlySerAlaVal	340
QY	1220	TGATGTATAGCATGATGATGAGAGGGTCTCTCTTGGTCCATATATCCACAGGAT	1279
DB	341	CysMetTyrSerMetSerAspValArgValPheLeuGlyProTyrAlaHisArgAsp	360
QY	1280	GGACCCAACTATCAATCGGTGCTTATCAAGGAAGAGTCCCTATCCAGGCCAGAACT	1339
DB	361	GlyProAsnTyrGlnTrpValProTyrGlnGlyArgValProTyrProArgProGlyThr	380
QY	1340	TGTCGCCGCAAAACATTTGGTGTGTTTGTACTCTACAAGAGCTTCTCATGATGTATA	1399
DB	381	CysProSerLysThrPheGlyGlyPheAspSerThrLysAspLeuProAspAspValIle	400
QY	1400	ACCTTTGCAAGAAGTATCCAGCCATGTACAAATCCAGTGTTCCTATGAACATCCGCCA	1459
DB	401	ThrPheAlaArgSerHisProAlaMetTyrAsnProValPheProMetAsnAsnArgPro	420
QY	1460	ATAGTGTATCAAAACCGGATGTAATTTACAAATTTACAAATTTGCTAGACCGAGTAT	1519
DB	421	IleValIleLysThrAspValAsnTyrGlnPheThrGlnIleValValAspArgValAsp	440
QY	1520	GCAGAGATGCAGATGATGTTATGTTTATCGGAACAGATGTTGGGACCGTCTTTAAA	1579
DB	441	AlaGluAspGlyGlnTyrAspValMetPheIleGlyThrAspValGlyThrValLeuLys	460
QY	1580	GTAGTTTCAATTCCTAAGGAGACTTGGTATGATTTAGAGAGAGTCTCTGCGAAGAAATG	1639
DB	461	ValValSerIleProLysGluThrTyrAspLeuGluGluValLeuLeuGluMet	480
QY	1640	ACAGTTTTCGGNACCGACTGCTATTCAGCAATGAGCTTTCCTACTAAGCAGCAACA	1699
DB	481	ThrValPheArgGluProThrAlaIleSerAlaMetGluLeuSerThrLysGlnGlnGln	500
QY	1700	CTATATATTTGGTTCAACGGCTGGGGTTGCCAGCTCCCTTTACACCGGTGTGATTTAC	1759
DB	501	LeuTyrIleGlySerThrAlaGlyValAlaGlnLeuProLeuHisArgCysAspIleTyr	520
QY	1760	GGGAAACCGTGTCTGAGTGTTCCTCGCCGAGACCTTACTGTCTGGGTGGTCT	1819
DB	521	GlyLysAlaCysAlaGluCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlySer	540
QY	1820	GCATGTTCTCGCTATTTTCCACTGCAAAAGAGACGACAGCAGCAAGATATATGAAT	1879
DB	541	AlaCysSerArgTyrPheProThrAlaLysArgArgThrArgGlnAspIleArgAsn	560

```

QY 1880 GGAGACCCACTGACTCTGTTTACAGCTTACACCATGATTAATCACCATGGCCACAGCCCT 1939
Db 561 GlyAspProLeuThrHisCysSerAspLeuHisHisAspAsnHisHisGlyHisSerPro 580
QY 1940 GAAGAGAGAAATCATCTGCTGTAGAGATAGTACACATTTTTCGAATGTCAGTCCGAAG 1999
Db 581 GluGluArgGilelleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 600
QY 2000 TGCAGAGAGCGCTGCTCTATTGGCAATTCCAGAGCGGAAATGAAGAGCGAAAGAGAG 2059
Db 601 SerGlnArgAlaLeuValTyrTrpGlnPheGlnArgArgAsnGluGluArgLysGluGlu 620
QY 2060 ATCAGAGTGGATCATCATATCATCAGGACAGATCAAGCCCTTCTGCTAGTACTACAA 2119
Db 621 IleArgValAspAspHisIleIleArgThrAspGlnGlyLeuLeuLeuArgSerLeuGln 640
QY 2120 CAGAAGCAATCAGGCAATTACCTCTGCCATGGGTGGAAACATGGGTTCATACAAACTCTT 2179
Db 641 GlnLysAspSerGlyAsnTyrLeuCysHisAlaValGluHisGlyPheIleGlnThrLeu 660
QY 2180 CTTAAGGTAACTGGAAGTCATTGACACAGAGCATTTGGAAGACTTCTTCTATTAAGAT 2239
Db 661 LeuLysValThrLeuGluValIleAspThrGluHisLeuGluGluLeuHisLysAsp 680
QY 2240 GATGATGGAGATGGCTCTAAGACCAAGAAATGTCCAATAGCATGACACCTAGCCAGAAG 2299
Db 681 AspAspGlyAspGlySerLysThrLysGluMetSerAsnSerMetThrProSerGlnLys 700
QY 2300 GTCTGTACAGAGACTTCATGAGCTCATCAACCCCAATCTCAACACGATGATGAG 2359
Db 701 ValTrpTyrArgAspPheMetGlnLeuIleAsnHisProAsnLeuAsnThrMetAspGlu 720
QY 2360 TTCTGTGAACAGTTTGGAAAGGACCGAACAACACGTCGGCAAGGCCAGGACATACC 2419
Db 721 PheCysGluGlnValTrpLysArgAspArgLysGlnArgGlnArgProGlyHisThr 740
QY 2420 CCAGGGAACAGTAACAAATGGAGACACTTACAGAAATAAGAAAGGTAGAAACAGGAGG 2479
Db 741 ProGlyAsnSerAsnLysTrpLysHisLeuGlnGluAsnLysLysGlyArgAsnArgArg 760
QY 2480 ACCAGCAATTGAGAGGGCACCCAGGAGTGTC 2512
Db 761 ThrHisGluPheGluArgAlaProArgSerVal 771

RESULT 2
US-10-262-538-10
; Sequence 10, Application US/10262538
; Publication No. US20030113324A1
; GENERAL INFORMATION:
; APPLICANT: Alitalia et al
; TITLE OF INVENTION: NEUROFILIN/VEGF-C/VEGFR-3 MATERIALS AND METHODS
; FILE REFERENCES: 28967/37564
; CURRENT APPLICATION NUMBER: US/10/262,538
; CURRENT FILING DATE: 2002-09-30
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 771
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-262-538-10

Alignment Scores:
Pred. No.: 0 Length: 771
Score: 4201.00 Matches: 771
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 85.80% Indels: 0
DB: 14 Gaps: 0

US-09-774-490-1 (1-2709) x US-10-262-538-10 (1-771)
QY 200 ATGGGCTGGTAACTAGGATTGTCCTTTCTGGGGAGTATTACTTACAGCAGAGCA 259

```

```

Db 1 MetGlyTrpLeuThrArgIleValCysLeuPheTrpGlyValLeuLeuThrAlaArgAla 20
QY 260 AACTATCAGAAATGGGAAGCAATGTCCCAAGGCTGAAATATCTCTCAACAAGAAATTTTG 319
Db 21 AsnTyrGlnAsnGlyLysAsnValProArgLeuLysLeuSerTyrLysGluMetLeu 40
QY 320 GAATCCCAATATGTGATCATTCTTCATGGCTTGGCCAAACAGCTCCAGTTATCATACCTC 379
Db 41 GluSerAsnValIleThrPheAsnGlyLeuAlaAsnSerSerSerTyrHisThrPhe 60
QY 380 CTTTGTGATGAGGACCGAGTAGGCTGTATGTTGGACAAAGGATCACATATTTTCATTC 439
Db 61 LeuLeuAspGluLysArgSerArgLeuTyrValGlyAlaLysAspHisIlePheSerPhe 80
QY 440 GACCTGTTAATATCAAGGATTTTCAAAAGATTGTGTGGCCAGTATCTTACACCAGAAGA 499
Db 81 AspLeuValAsnIleLysAspPheGlnLysIleValTrpProValSerTyrThrArgArg 100
QY 500 GATCAATGCAAGTGGGCTGGAAAGACATCTCTGAAAGAATGTGCTAATTTTCATCAAGGTA 559
Db 101 AspGluCysLysTrpAlaGlyLysAspIleLeuLysGluCysAlaAsnPheIleLysVal 120
QY 560 CTTAAGGCATATATCAGACTCACTTGTAGCCTGTGGAACGGGGGCTTTTCATCCAATT 619
Db 121 LeuLysAlaTyrAsnGlnThrHisLeuTyrAlaCysGlyThrGlyAlaPheHisProile 140
QY 620 TGCACCTACATTGAAATGGACATCATCTGAGGACAAATATTTTAAGCTGGAGAACTCA 679
Db 141 CysThrTyrIleGluIleGlyHisHisProGluAspAsnIlePheLysLeuGluAsnSer 160
QY 680 CATTTTCAAAACGGCGCTGGGAAGAGTCCCATATCACCCCTAAGCTGTGACAGCATCCCTT 739
Db 161 HisPheGluAsnGlyArgGlyLysSerProTyrAspProLysLeuLeuThrAlaSerLeu 180
QY 740 TTAATAGATGAGAAATATATCTCTGGAACCTGACGCTGATTTTATGGGGCAGACTTCCT 799
Db 181 LeuIleAspGlyGluLeuTyrSerGlyThrAlaAlaAspPheMetGlyArgAspPheAla 200
QY 800 ATCTTCGGAACCTTTGGGCACCCACCACCAATCAGGACAGACAGCATGATTTCCAGGTGG 859
Db 201 IlePheArgThrLeuGlyHisHisIleProIleArgThrGluGlnHisAspSerArgTrp 220
QY 860 CTCAATGATCCAAAGTTTCATTAGTGGCCACCTCATCTCAGAGAGTGACAATCTCTGAAGAT 919
Db 221 LeuAsnAspProLysPheIleSerAlaHisLeuIleSerGluSerAspAsnProGluAsp 240
QY 920 GACAAAGTATATCTTTTCTCCGTGAAATGCATAGATGAGAGACACTCTGGAAAGCT 979
Db 241 AspLysValTyrPhePheArgGluAsnAlaIleAspGlyGluHisSerGlyLysAla 260
QY 980 ACTCACGCTAGATAGGTTCAGATATGCAAGAATGACTTTGGAGGGCACAGAAGTCTGGTG 1039
Db 261 ThrHisAlaArgIleGlyGlnIleCysLysAsnAspPheGlyGlyHisArgSerLeuVal 280
QY 1040 AATAAATGGACAACATTCCTCAAGCTCGTCTGATTTGCTCAGTGGCCAGGTCGCAAAATGGC 1099
Db 281 AsnLysTrpThrThrPheLeuLysAlaArgLeuIleCysSerValProGlyProAsnGly 300
QY 1100 ATTGCACTCATTTTGTATGTAAGTCTCAGGATGTATCTCTTAATGACTTTTAAAGATCCTAAA 1159
Db 301 IleAspThrHisPheAspGluLeuGlnAspValPheLeuMetAsnPheLysAspProLys 320
QY 1160 AATCCAGTTGTATGGAGTGTTTTACGACTTCCAGTAACTATTTTCAAGGGATCAGCCGTG 1219
Db 321 AsnProValValTyrGlyValPheThrThrSerSerAsnIlePheLysGlySerAlaVal 340
QY 1220 TGTATGTACATGAGTGTGTGAGAGGCTGTTCTTGGTCCATATGCCACAGGAT 1279
Db 341 CysMetTyrSerMetSerAspValArgValPheLeuGlyProTyrAlaHisArgAsp 360
QY 1280 GGACCCCACTATCAATGGTGCCTTATCAAGGAAGAGTCCCTTATCCACGCGCCAGGAAC 1339

```

Thu Sep 23 08:54:06 2004

361 GlyProAsnTyrGlnTrpValProTyrGlnArgValProTyrProArgProGlyThr 380
 1340 TGTCACGAGAAACATTTGGTGGTTTGAATCTCTACAAAGGACCTTCTGTGATGATTATA 1399
 381 CysProSerLysThrPheGlyGlyPheAspSerThrLysAspLeuProAspValIle 400
 1400 ACCTTTGCAAGAGCATCCAGCCATGACAAATCCAGTGTTCCTATGAACAATCGCCCA 1459
 401 ThrPheAlaArgSerHisProAlaMetTyrAsnProValPheProMetAsnAsnArgPro 420
 1460 ATAGTCATCAAAACCGATGTAATATCAATATCAATATCAAAATTCGTAGACCGAGTGAT 1519
 421 IleValIleLysThrAspValAsnTyrGlnPheThrGlnIleValValAspArgValAsp 440
 1520 CGAGAGATGGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1579
 441 AlaGluAspGlyGlnTyrAspValMetPheIleGlyThrAspValGlyThrValLeuLys 460
 1580 GTAGTTTCAATTCCTAAGAGACTTGTGATGATGATGATGATGATGATGATGATGATGAT 1639
 461 ValValSerIleProLysGlnThrTrpTyrAspLeuGluValLeuLeuGluMet 480
 1640 ACAGTTTTCGGAACCGACTGCTATTCAGCAATGGAGCTTCCACTAAGCAGCAACA 1699
 481 ThrValPheArgGluProThrAlaIleSerAlaMetGluLeuSerThrLysGlnGln 500
 1700 CTATATATTGTTCAACGCTGGGCTGCCAGCTCCCTTTACACCGGTGTGATATTAC 1759
 501 LeuTyrIleGlySerThrAlaGlyValAlaGlnLeuProLeuHisArgCysAspIleTyr 520
 1760 GGAAGACGCTGTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1819
 521 GlyLysAlaCysAlaGluCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlySer 540
 1820 GCATGTTCTCGCTATTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1879
 541 AlaCysSerArgTyrPheProThrAlaLysArgThrArgGlnAspIleArgAsn 560
 1880 GGAGACCCACTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1939
 561 GlyAspProLeuThrHisCysSerAspLeuHisAspAsnHisGlyHisSerPro 580
 1940 GAAGAGAGATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1999
 581 GluGluArgIleIleTyrGlyValGluAsnSerSerThrPheLeuGluCysSerProLys 600
 2000 TGCAGAGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2059
 601 SerGlnArgAlaLeuValTyrTrpGlnPheGlnArgArgAsnGluGluArgLysGluGlu 620
 2060 ATCAGAGTGGATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 2119
 621 IleArgValAspAspHisIleIleArgThrAspGlnGlyLeuLeuLeuArgSerLeuGln 640
 2120 CAGAAGGATTCAGGCAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2179
 641 GlnLysAspSerGlyAsnTyrLeuCysHisAlaValGluHisGlyPheIleGlnThrLeu 660
 2180 CTTAAGTAAACCTGGAATGCTATTCACAGAGCATTTGGAGAACTTCTCTCATTAAGAT 2239
 661 LeuLysValThrLeuGluValIleAspThrGluHisLeuGluGluLeuLeuHisLysAsp 680
 2240 GATGATGGAGATGCTCTAAGACCAAGAAAGTCAATAGCATGACACCTAGCCAGAG 2299
 681 AspAspGlyAspGlySerLysThrLysGluMetSerAsnSerMetThrProSerGlnLys 700
 2300 GTCTGTACAGACTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2359
 701 ValTyrArgAspPheMetGlnLeuIleAsnHisProAsnLeuAsnThrMetAspGlu 720
 2360 TTCTGTGAACAGTTTGGAAAGGACCGAAGACACGCTCGCAAGCCAGGACATACC 2419
 721 PheCysGluGlnValTrpLysArgAspArgLysGlnArgGlnArgProGlyHisThr 740

QY 2420 CCAGGAAACAGTAACAAATGGAAGCACTTACAGAAAATAAGAAAGGTAGAAACAGGAGG 2479
 Db 741 ProGlyAsnSerAsnLysTrpLysHisLeuGlnGluAsnLysLysGlyArgAsnArgArg 760
 QY 2480 ACCACGAATTTGAGAGGCGACCCAGGAGTGTC 2512
 Db 761 ThrHisGluPheGluArgAlaProArgSerVal 771

RESULT 3

US-10-067-632-54
 ; Sequence 54, Application US/10067632
 ; Publication No. US20030166849A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Goodman, Corey S.
 ; Kolodkin, Alex L.
 ; Matthes, David
 ; Beatley, David R.
 ; O'Connor, Timothy
 ; TITLE OF INVENTION: The Semaphorin Gene Family
 ; NUMBER OF SEQUENCES: 100
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
 ; STREET: 268 Bush Street, Suite 3200
 ; CITY: San Francisco
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94104
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/067,632
 ; FILING DATE: 04-Feb-2002
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/060,610
 ; FILING DATE: <Unknown>
 ; APPLICATION NUMBER: 08/835,268
 ; FILING DATE: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Osman, Richard A.
 ; REGISTRATION NUMBER: 36,627
 ; REFERENCE/DOCKET NUMBER: B94-002-1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415)343-4341
 ; TELEFAX: (415) 343-4342
 ; TELEX: <Unknown>
 ; INFORMATION FOR SEQ ID NO: 54:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 771 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 54:
 US-10-067-632-54

Alignment Scores:
 Pred. No.: 0 Length: 771
 Score: 4201.00 Matches: 771
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 85.80% Indels: 0
 DB: 14 Gaps: 0

US-09-774-490-1 (1-2709) x US-10-067-632-54 (1-771)

QY 200 ATGGCTGGTAACTAGGATGCTCTTTCTGGGAGTATTACTTACAGCAAGACGA 259
 Db 1 MetGlyTrpLeuThrArgIleValCysLeuPheTrpGlyValLeuLeuThrAlaArgAla 20

QY 260 AACTATCAGATGGGAAGAACAAATGTGCGAAGGCTGAAATATATCTTACAAAGAAATGTTG 319
Db 21 AsnTyrGlnAsnGlyLysAsnValProArgLeuLysLeuSerTyrLysGluMetLeu 40
QY 320 GAATCAACAATGTGATCACTTTCAATGCTTGGCCACACAGCTCCAGTATCATACCTTC 379
Db 41 GluSerAsnAsnValIleThrPheAsnGlyLeuAlaAsnSerSerTyrHisThrPhe 60
QY 380 CTTTGGATGAGAACGGAGTAGGCTGTATGTGGAGCAAGGATCAATATTTTCATC 439
Db 61 LeuLeuAspGluGluArgSerArgLeuTyrValGlyAlaLysAspHisIlePheSerPhe 80
QY 440 GACCTGTTAATATCAAGGATTTCAAAAGATTGTGTGCCAGTATCTTACACCAAGAAGA 499
Db 81 AspLeuValAsnIleLysAspPheGlnLysIleValTrpProValSerTyrThrArgArg 100
QY 500 GATGAATCAAGTGGCTCGAAAGACATCCCTGAAAGATGTGCTAATTTTCATCAAGGTA 559
Db 101 AspGluCysLysTrpAlaGlyLysAspIleLeuLysGluCysAlaAsnPheIleLysVal 120
QY 560 CTTAAGGCATATATCAGACTCACTGTAGCTGTGACGCTGTGGACCGGGCTTTTCATCAATT 619
Db 121 LeuLysAlaTyrAsnGlnThrHisLeuTyrAlaCysGlyThrGlyAlaPheHisProIle 140
QY 620 TGCACCTCATATTGAAATTCGAATCATCTCTGAGGACAATATTTTAAAGCTGGAGAACTCA 679
Db 141 CysThrTyrIleGluIleGlyHisHisProGluAspAsnIlePheLysLeuGluAsnSer 160
QY 680 CATTTGAAAACGGCGTGGGAAGAGTCCATATGACCTTAAGCTGTGACAGATCCCTT 739
Db 161 HisPheGluAsnGlyArgGlyLysSerProTyrAspProLysLeuLeuThrAlaSerLeu 180
QY 740 TTAATAGATGGAGAATTATCTGGAATCTGGAATCTGAGCTGATTTATGGGCGAGCTTGT 799
Db 181 LeuIleAspGlyGluLeuTyrSerGlyThrAlaAlaAspPheMetGlyArgAspPheAla 200
QY 800 ATCTTCGGAACCTTGGGCACCAACCAATCAGACAGACAGCATGATTTCCAGGTGG 859
Db 201 IlePheArgThrLeuGlyHisHisProIleArgThrGluGlnHisAspSerArgTrp 220
QY 860 CTCATATGCCAAAGTTATAGTCCGACCTCATCTCAGAGTGACAACTCTCAAGT 919
Db 221 LeuAsnAspProLysPheIleSerAlaHisLeuIleSerGluSerAspAsnProGluAsp 240
QY 920 GACAAAGTATACTTTTCTTCGCTGAAAATGCAATAGATGGAGAACATCTCTGAAAAGCT 979
Db 241 AspLysValTyrPhePheArgGluAsnAlaIleAspGlyGluHisSerGlyLysAla 260
QY 980 ACTCAGCTAGATAGGTGAGATATGCCAAGATGACTTTGGAGGGCACAGAAGTCTGGTG 1039
Db 261 ThrHisAlaArgIleGlyGlnIleCysLysAsnAspPheGlyHisArgSerLeuVal 280
QY 1040 AATAAATGACACACTCTCTCAAGCTCTCTGATTTGCTCAGTGCAGGTCCTCAATGGC 1099
Db 281 AsnLysTrpThrThrPheLeuLysAlaArgLeuIleCysSerValProGlyProAsnGly 300
QY 1100 ATTGACACTCATTTGATGACTGACAGGATGATTCTTAATCAACTTTAAAGATCCTAAA 1159
Db 301 IleAspThrHisPheAspGluLeuGlnAspValPheLeuMetAsnPheLysAspProLys 320
QY 1160 AATCCAGTTGATATGAGTGTACGACTTCAGTAACTTTCAGGGATCCAGCGT 1219
Db 321 AsnProValValTyrGlyValPheThrThrSerSerAsnIlePheLysGlySerAlaVal 340
QY 1220 TGTATGTATAGCATGATGTAGAGAGGGTGTCTCTTGGTCCCATATGCCACAGGGAT 1279
Db 341 CysMetTyrSerMetSerAspValArgArgValPheLeuGlyProTyrAlaHisArgAsp 360
QY 1280 GGAACCAACTATCAATGGGTGCTTATCAAGAGAGTCCCTATCCACGGCCAGGAAGT 1339
Db 361 GlyProAsnTyrGlnTrpValProTyrGlnGlyArgValProTyrProArgProGlyThr 380
QY 1340 TGTCGCCAGCAAAACATTTGGTGGTTTGTACTCTTACAAAGGACCTTCTCTGATGATGTTATA 1399

Db 381 CysProSerLysThrPheGlyGlyPheAspSerThrLysAspLeuProAspValIle 400
QY 1400 ACCTTTTCAAGAAGTTCATCCAGCCATGTACAATCCAGTGTTCCTATGAACAATCGCCCA 1459
Db 401 ThrPheAlaArgSerHisProAlaMetTyrAsnProValPheProMetAsnAsnArgPro 420
QY 1460 ATAGTGATCAAAACGGATGTAAATTTATCAATTTACAAAATTTGCTAGACCCGATGGAT 1519
Db 421 IleValIleLysThrAspValAsnTyrGlnPheThrGlnIleValValAspArgValAsp 440
QY 1520 GCAGAAATGCAGACATATGATGTTATGTTTATCGGAACACAGATGTGGGACCGTCTTAAA 1579
Db 441 AlaGluAspGlyGlnTyrAspValMetPheIleGlyThrAspValGlyThrValLeuLys 460
QY 1580 GTAGTTTCAATTCCTAAGGAGACTGTGTATGATTTAGAAGAGTTCGTCTGGAGAAATG 1639
Db 461 ValValSerIleProLysGluThrTrpTyrAspLeuGluValLeuLeuGluMet 480
QY 1640 ACAGTTTTCGGGAACCGACTGTCTATTTACAGCAATGGAGCTTCCACTAAGCAGCAACAA 1699
Db 481 ThrValPheArgGluProThrAlaIleSerAlaMetGluLeuSerThrLysGlnGln 500
QY 1700 CTATATATTGGTCAACGGTGGGTTGCCAGCTCCCTTTTACACCGTGTGTATTTAC 1759
Db 501 LeuTyrIleGlySerThrAlaGlyValAlaGlnLeuProLeuHisArgCysAspIleTyr 520
QY 1760 GGGAAAGCTGTCTGAGTGTCTCCTCGCCGAGACCTTACTGTCTGGATGGTCT 1819
Db 521 GlyLysAlaCysAlaGluCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlySer 540
QY 1820 GCATGTTCTCGCTATTTTCCACTGCAAAAGAGACGCAAGACAGCAAGATATAAGAAAT 1879
Db 541 AlaCysSerArgTyrPheProThrAlaLysArgThrArgArgGlnAspIleArgAsn 560
QY 1880 GGAGACCCACTGACTCATCTGTTAGACTTACACCATGATATATCCATGCCACAGCCCT 1939
Db 561 GlyAspProLeuThrHisCysSerAspLeuHisAspAsnHisHisGlyHisSerPro 580
QY 1940 GAACAGAGATCATCTATGTGTAGAAATAGTAGACATTTTGGAAATGCAGTCCGAAG 1999
Db 581 GluGluArgIleIleTyrGlyValGluAsnSerSerThrPheLeuGluCysSerProLys 600
QY 2000 TCGCAGAGAGCGTGTCTATTGGCAATTCAGAGCGGAAATGAAGAGCGAAAGAGAG 2059
Db 601 SerGlnArgAlaLeuValTyrTrpGlnPheGlnArgArgAsnGluGluArgLysGluGlu 620
QY 2060 ATCAGAGTGGATGATCATATCATCAGGACAGATCAAGCGCTTCTGTCTACGTAGTCTACAA 2119
Db 621 IleArgValAspAspHisIleIleArgThrAspGlnGlyLeuLeuLeuArgSerLeuGln 640
QY 2120 CAGAAGGATTCAGGCAATTAACCTCTGCCATCGGTGGAAACATGGGTTTCATAAACTCTT 2179
Db 641 GlnLysAspSerGlyAsnTyrLeuCysHisAlaValGluHisGlyPheIleGlnThrLeu 660
QY 2180 CTTAAGGTAACTTGGAGTCAATGACAGACCATTTGGAAGACTTCTTCTATAAGAT 2239
Db 661 LeuLysValThrLeuGluValIleAspThrGluHisLeuGluGluLeuLeuHisLysAsp 680
QY 2240 GATCATGGAGATGGCTCTAAGACCAAAAGAAATGTCCAATAGCATGACACCTAGCCAGAAG 2299
Db 681 AspAspGlyAspGlySerLysThrLysGluMetSerAsnSerMetThrProSerGlnLys 700
QY 2300 GTCTGGTACAGAGACTTCATGCGAGCTCATCAACCCCAATCTCAACAGATGGATGAG 2359
Db 701 ValTrpTyrArgAspPheMetGlnLeuIleAsnHisProAsnLeuAsnThrMetAspGlu 720
QY 2360 TTTCTGTGACACAAGTTTGGAAAAGGACCGGAAAACAACGTCGGCAAGGCCAGGACATACC 2419
Db 721 PheCysGluGlnValTrpLysArgAspArgLysGlnArgGlnArgProGlyHisThr 740
QY 2420 CCAGGGAACAGTAACAAATGGAACACTTCAAGAAAATAGAAAGTGAACAAACAGGAGG 2479

Db 741 ProGlyAsnSerAsnLysTrpLysHisLeuGlnGluAsnLysLysGlyArgAsnArg 760

QY 2480 ACCACGAATTGAGAGGCGCCAGGAGTCTC 2512

Db 761 ThrHisGluPheGluArgAlaProArgSerVal 771

RESULT 4

US-10-247-671-164

Sequence 164, Application US/10247671

Publication No. US20030194721A1

GENERAL INFORMATION:

APPLICANT: Mikita, Thomas

APPLICANT: Shiffman, Dov

APPLICANT: Porter, Gordon, J.

APPLICANT: Kaser, Matthew R.

FILE OF INVENTION: GENES EXPRESSED IN TREATED FOAM CELLS

FILE REFERENCE: PA-0050 US

CURRENT APPLICATION NUMBER: US/10/247,671

CURRENT FILING DATE: 2002-09-18

PRIOR APPLICATION NUMBER: 60/323,784

PRIOR FILING DATE: 2001-09-19

NUMBER OF SEQ ID NOS: 186

SOFTWARE: PERL Program

SEQ ID NO 164

LENGTH: 771

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc_feature

OTHER INFORMATION: Incyte ID No. US20030194721A1 1930967CD1

US-10-247-671-164

Alignment Scores:

Pred. No.: 0 Length: 771

Score: 4201.00 Matches: 771

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 85.80% Indels: 0

DB: 14 Gaps: 0

US-09-774-490-1 (1-2709) x US-10-247-671-164 (1-771)

QY 200 ATGGCTGTTAACTAGATTCTCTGCTTTCTGGGAGTATTACTTACAGCAGACGA 259

Db 1 MetGlyTrpLeuThrArgIleValCysLeuPheTrpGlyValLeuLeuThrAlaArgAla 20

QY 260 AACTATCAGAAATGGGAAGAACAAATGTGCCAAGCTGAAATATCTCAAAAGAAATGTTG 319

Db 21 AsnTyrGlnAsnGlyLysAsnAsnValProArgLeuLysLeuSerTyrLysGluMetLeu 40

QY 320 GAATCAACAATGTGATCACTTCAATGGCTTGGCCACAGCTCAGTATCATACCTTC 379

Db 41 GluSerAsnValIleThrPheAsnGlyLeuAlaAsnSerSerTyrHisThrPhe 60

QY 380 CTTTGGATGAGAACGGAGTAGGCTGTATGTTGGAGCAAGATCATATTTTCATTC 439

Db 61 LeuLeuAspGluGluArgSerArgLeuTyrValGlyAlaLysAspHisIlePheSerPhe 80

QY 440 GACCTGTTTAAATATCAAGGATTTTCAAAAGATTGTGTGCCAGTATCTTACACAGAGA 499

Db 81 AspLeuValAsnIleLysAspPheGlnLysIleValTrpProValSerTyrThrArgArg 100

QY 500 GATGAATGAGTGGCTGGAAAGACATCTCTGAAGATGCTTAATTTTCATCAAGGTA 559

Db 101 AspGluCysLysTrpAlaGlyLysAspIleLeuLysGluCysAlaAsnPheIleLysVal 120

QY 560 CTTAAGGCATATAATCAGACTCACITGTACGGCTGTGGAAACGGGGCTTTTCATCCAATT 619

Db 121 LeuLysAlaTyrAsnGlnThrHisLeuTyrAlaCysGlyThrGlyAlaPheHisProIle 140

QY 620 TGCACCTACATTGAATTTGGACATCATCTGAGGACATATTTTAACTGGAGACTCA 679

Db 141 CysThrTyrIleGluIleGlyHisHisProGluAspAsnIlePheLysLeuGluAsnSer 160

QY 680 CATTTTGAAAACGGCCGTGGGAGAGTCCATATGACCCTTAAGCTGCTCAGACATCCCTT 739

Db 161 HisPheGluAsnGlyArgGlyLysSerProTyrAspProLysLeuLeuThrAlaSerLeu 180

QY 740 TTAATAGATGGAGAAATTATCTCTGGAACCTGAGCTGATTTTATGGGGCGAGACTTCT 799

Db 181 LeuIleAspGlyGluLeuTyrSerGlyThrAlaAlaAspPheMetGlyArgAspPheAla 200

QY 800 ATCTTCGGAACCTTGGGCGACACACCACTCAAGTTCAGAGAGTGCACAACTCTCAAGTGG 859

Db 201 IlePheArgThrLeuGlyHisHisIleAspIleArgThrGluGlnHisAspSerArgTrp 220

QY 860 CTCAATGATCCAAAGTTTCATTAGTCCCACTCTCATCTCAGAGAGTGCACAACTCTCAAG 919

Db 221 LeuAsnAspProLysPheIleSerAlaHisLeuIleSerGluSerAspAsnProGluAsp 240

QY 920 GACAAAGTATATCTTTCTTCGCGTGAATCAATAGTGGAGACACCTCTGGAAAGCT 979

Db 241 AspLysValTyrPhePhePheArgGluAsnAlaIleAspGlyGluHisSerGlyLysAla 260

QY 980 ACTCAGCTAGAAATAGTACAGATATGCAAGATGCTTTGGAGGCGACAGAGTCTGGTG 1039

Db 261 ThrHisAlaArgIleGlyGlnIleCysLysAsnAspPheGlyGlyHisArgSerLeuVal 280

QY 1040 AATAAATGACAAACATCTCTCAAGCTGCTCTGATTTGCTCAGTCCAGTCCAGTCCAAATGCC 1099

Db 281 AsnLysTrpThrPheLeuLysAlaArgLeuIleCysSerValProGlyProAsnGly 300

QY 1100 ATTGACACTCATTGATCACTGAGGATGATTTCTTAATCAACTTTTAAAGATCCTAAA 1159

Db 301 IleAspThrHisPheAspGluLeuGlnAspValPheLeuMetAsnPhelysAspProLys 320

QY 1160 AATCCAGTTGTATATGAGTGTTTACGACTTCCAGTAACTTTTCAAGGATCAGCCCGTG 1219

Db 321 AsnProValValTyrGlyValPheThrThrSerSerAsnIlePheLysGlySerAlaVal 340

QY 1220 TGTATGTATAGCATGATGATGAGAGGTTTCTTGTGTCATATGCCCCACAGGAT 1279

Db 341 CysMetTyrSerMetSerAspValArgValPheLeuGlyProTyrAlaHisArgAsp 360

QY 1280 GGACCCAACTATCAATGGGTGCTTTATCAAGGAAGAGTCCCTATCCAGGCGCAGAACT 1339

Db 361 GlyProAsnTyrGlnTrpValProTyrGlnGlyArgValProTyrProArgProGlyThr 380

QY 1340 TGTCCCGCAAAACATTTGCTGTTTGTACTCTACAGAGACCTTCTCTGATCATGTATA 1399

Db 381 CysProSerLysThrPheGlyGlyPheAspSerThrLysAspLeuProAspValIle 400

QY 1400 ACCTTTGCAAGAGTCACTCAGCCATGTACAATCCAGTGTTCCTATGAACTCAATCGCCA 1459

Db 401 ThrPheAlaArgSerHisProAlaMetTyrAsnProValPheProMetAsnAsnArgPro 420

QY 1460 ATAGTGATCAAAACGAGTGTAAATATCAATTTACAAATTTGTGTAGACCGAGTGGAT 1519

Db 421 IleValIleLysThrAspValAsnTyrGlnPheThrGlnIleValValAspArgValAsp 440

QY 1520 GCAGAGATGGACAGATGATGTATGTTTATCGGAACAGATGTTGGGACCGTCTCTTAA 1579

Db 441 AlaGluAspGlyGlnTyrAspValMetPheIleGlyThrAspValGlyThrValLeuLys 460

QY 1580 GTAGTTTCAATTCCTAAGGAGACTTGGTATGATTTTGAAGAGTGTCTGCTGAAGAAATG 1639

Db 461 ValValSerIleProLysGluThrTrpTyrAspLeuGluGluValLeuLeuGluMet 480

QY 1640 ACAGTTTTTGGGAAACCGACTGCTATTTTCAGCAATCGAGCTTCCACTAAGCAGAACAA 1699

Db 481 ThrValPheArgGluProThrAlaIleSerAlaMetGluLeuSerThrLysGlnGlnGln 500

QY 1700 CTATATATTGGTTCAACGGCTGGGGTGGCCAGCTCCCTTTTACCGGTGTGATATTAC 1759

Db 501 LeuTyrIleGlySerThrAlaGlyValAlaGlnLeuProLeuHisArgCysAspIleTyr 520

```

QY 1760 GGGAAAGCGTGTGCTGAGTGTGCTCGCCGAGACCCCTTACTGTGCTTGGGATGTTCT 1819
Db 521 GlyLysAlaCysAlaGluCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlySer 540
QY 1820 GCATGTTCTCGGTATTTTCCCACTGCAAGACACCAAGACGACAAAGATATAGAAT 1879
Db 541 AlaCysSerArgTyrPheProThrAlaLysArgArgThrArgGlnAspIleArgAsn 560
QY 1880 GGAGACCCACTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1939
Db 561 GlyAspProLeuThrHisCysSerAspLeuHisHisAspAsnHisHisGlyHisSerPro 580
QY 1940 GAAGAGAGAAATCATCTATGCTGTAGAGATAGATAGATAGATAGATAGATAGATAGAT 1999
Db 581 GluGluArgIleIleTyrGlyValGluAsnSerSerThrPheLeuGluCysSerProLys 600
QY 2000 TCGAGAGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2059
Db 601 SerGlnArgAlaLeuValTyrTrpGlnPheGlnArgArgAsnGluGluArgLysGluGlu 620
QY 2060 ATCAGAGTGGATGATCATATCATCATCATCATCATCATCATCATCATCATCATCATCAT 2119
Db 621 IleArgValAspAspHisIleIleArgThrAspGlnGlyLeuLeuLeuArgSerLeuGln 640
QY 2120 CAGAAGGATTACGCAATACCTCTGCCATGCGGTGGACATGGGTTCATACAAACTCTT 2179
Db 641 GlnLysAspSerGlyAsnTyrLeuCysHisAlaValGluHisGlyPheIleGlnThrLeu 660
QY 2180 CTTAAGGTAACTGGAAGTCACTGACACAGAGCATTTGGAAGAACTTCTTCATAGAAT 2239
Db 661 LeuLysValThrLeuGluValIleAspThrGluHisLeuGluGluLeuHisLysAsp 680
QY 2240 GATGATGGAGATGGCTTCAAGCAACCAAGAAATGTCCAATAGCATGACACTAGCCAGAAG 2299
Db 681 AspAspGlyAspGlySerLysThrLysGluMetSerAsnSerMetThrProSerGlnLys 700
QY 2300 GTCTGTGACAGACTTCATGAGCTCATCAACCCCACTCAACCCCACTCAACCCCACTCAAC 2359
Db 701 ValTrpTyrArgAspPheMetGlnLeuIleAsnHisProAsnLeuAsnThrMetAspGlu 720
QY 2360 TTCTGTGACAAAGTTTGGAAAGGACCGAAACACACGTCGCGCAAGGCGGACATACC 2419
Db 721 PheCysGluGlnValTrpLysArgAspArgLysGlnArgArgGlnArgProGlyHisThr 740
QY 2420 CCAGGGAACAGTAACAAATGGAAGCACTTACAGAAATTAAGAAAGTGAAGAACAGGAGG 2479
Db 741 ProGlyAsnSerAsnLysTrpLysHisLeuGlnGlnLysLysLysGlyArgAsnArgArg 760
QY 2480 ACCACGAATTTGAGAGGCGCCAGGAGTGTC 2512
Db 761 ThrHisGluPheGluArgAlaProArgSerVal 771

```

RESULT 5

US-10-320-769-3

Sequence 3, Application US/10320769

Publication No. US20030158402A1

GENERAL INFORMATION:

APPLICANT: HALL, Kathryn T.

APPLICANT: FREEMAN, Gordon J.

APPLICANT: SCHULTZE, Joachim L.

APPLICANT: BOUSSIERIS, Vassiliki

APPLICANT: NADLER, Lee M.

TITLE OF INVENTION: NUCLEIC ACIDS ENCODING CD100 MOLECULES

FILE REFERENCE: DFN-005CPA2.

CURRENT APPLICATION NUMBER: US/10/320,769

PRIOR FILING DATE: 2002-12-16

PRIOR FILING DATE: 1995-11-09

NUMBER OF SEQ ID NOS: 7

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 3

LENGTH: 655

TYPE: PRT

ORGANISM: Homo sapiens

US-10-320-769-3

Alignment Scores:

Pred. No.: 0 Length: 655

Score: 3568.00 Matches: 655

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 72.88% Indels: 0

DB: 14 Gaps: 0

US-09-774-490-1 (1-2709) x US-10-320-769-3 (1-655)

```

QY 200 ATGGCTGGTAACTAGGATGTCTGCTTTCTGGGAGTATTACTTACAGCAAGACA 259
Db 1 MetGlyTrpLeuThrArgIleValCysLeuPheTrpGlyValLeuLeuThrAlaArgAla 20
QY 260 AACTATCAGAAATGGGAAGAACAATGTGCCAAGCTGAAATATCTCTCAAGAAGATGTTG 319
Db 21 AsnTyrGlnAsnGlyLysAsnAsnValProArgLeuLysLeuSerTyrLysGluMetLeu 40
QY 320 GAATCCCAACAATGTGATCACTTTCAATGGCTTGGCCAAACAGCTCCAGTTATCATACCTTC 379
Db 41 GluSerAsnAsnValIleThrPheAsnGlyLeuAlaAsnSerSerSerTyrHisThrPhe 60
QY 380 CTTTGGATGAGGAACCGAGTAGCTGTATGTGGAGCAAGGATCATATTTTCATTC 439
Db 61 LeuLeuAspGluGluArgSerArgLeuTyrValGlyAlaLysAspHisIlePheSerPhe 80
QY 440 GACCTGCTTAATATCAGAGGATTTTCAAAAGATGTGTGGCCAGTATCTTACACCAGAGA 499
Db 81 AspLeuValAsnIleLysAspPheGlnLysIleValTrpValSerTyrThrArgArg 100
QY 500 GATCAATGCAAGTGGGTGGAAAAGACATCTCTGAGGACAAATATTTTAAAGCTGGAGAACTCA 559
Db 101 AspGluCysLysTrpAlaGlyLysAspIleLeuLysGluCysAlaAsnPheIleLysVal 120
QY 560 CTTAAGGCATATAATCAGACTCCTTGTAGCCCTGTGCGGAGCGGGGCTTTTCATCCATT 619
Db 121 LeuLysAlaTyrAsnGlnThrHisLeuTyrAlaCysGlyThrGlyAlaPheHisProIle 140
QY 620 TGCACCTACATTTGAAATGGACATCATCTCTGAGGACAAATATTTTAAAGCTGGAGAACTCA 679
Db 141 CysThrTyrIleGluIleGlyHisHisProGluAspAsnIlePheLysLeuGluAsnSer 160
QY 680 CATTTTGAAGAACCGCCCTGGGAAGAGTCCATATGACCCCTAAGCTGTGACAGCATCCCTT 739
Db 161 HisPheGluAsnGlyArgGlyLysSerProTyrAspProLysLeuLeuThrAlaSerLeu 180
QY 740 TTAATAGATGAGAAATATATCTCTGGAACCTGCGAGTCTGATTTTATGGGCGGAGACTTTGCT 799
Db 181 LeuIleAspGlyGluLeuTyrSerGlyThrAlaAlaAspPheMetGlyArgAspPheAla 200
QY 800 ATCTTCCGAACCTTTGGGCACACCACCAATCAGGACAGACAGCATGATTCCAGGTGG 859
Db 201 IlePheArgThrLeuGlyHisHisHisProIleArgThrGluGlnHisAspSerArgTrp 220
QY 860 CTCATATGATCCAAAGTTTCATAGTGGCCCACTCATCTCTCAGAGAGTGCATCTCAGAGAT 919
Db 221 LeuAsnAspProLysPheIleSerAlaHisLeuLysSerGluSerAspAsnProGluAsp 240
QY 920 GACAAAGTATATCTTTTCTCCGTGAAAATGCAATAGATGGAACAACACTCTGGAAGAAAGCT 979
Db 241 AspLysValTyrPhePheArgGluAsnAlaIleAspGlyGluHisSerGlyLysAla 260
QY 980 ACTCAGCGCTAGAATAGGTACAGATATGCAAGATGACATTTGGAGGGCGCAGAGTCTGGTG 1039
Db 261 ThrHisAlaArgIleGlyGlnIleCysLysAsnAspPheGlyGlyHisArgSerLeuVal 280
QY 1040 AATAAATGGACAACATCTCTCAAGCTCGTCTGATTTTGTCTCAGTGCAGGTCCTCAATGGC 1099
Db 281 AsnLysTrpThrThrPheLeuLysAlaArgLeuIleCysSerValProGlyProAsnGly 300

```

QY 1100 ATTGACACTCAATTTGATGAAGTGGAGTGTATCTCTAATGAACCTTTAAGATCCTAAA 1159
Dd |||||
QY 301 TleAspThrHisPheAspGluLeuGlnAspValPheLeuMetAsnPheLysAspProLys 320
Dd |||||
QY 1160 AATCCAGTTGTATATGGAGTGTTCACGACTTCCAGTAACATTTTCAAGGGATCAGCGGTG 1219
Dd |||||
QY 321 AsnProValValTyrGlyValPheThrThrSerSerAsnIlePheLysGlySerAlaVal 340
Dd |||||
QY 1220 TGTATGTATAGCATGAGTGTAGAGAGGGTGTTCCTGTGTCATATGCCACAGGAT 1279
Dd |||||
QY 341 CysMetTyrSerMetSerAspValArgArgValPheLeuGlyProTyrAlaHisArgAsp 360
Dd |||||
QY 1280 GGACCACTATCAATGGTGCTTATCAAGAGAGTCCCTATCCACGCCACGAGAACT 1339
Dd |||||
QY 361 GlyProAsnTyrGlnTrpValProTyrGlnGlyArgValProTyrProArgProGlyThr 380
Dd |||||
QY 1340 TGTCCAGCAAAACATTTGGTGGTTTTCACCTCTACAAAAGGACCTTCTCTGATGATGTATA 1399
Dd |||||
QY 381 CysProSerLysThrPheGlyGlyPheAspSerThrLysAspLeuProAspAspValIle 400
Dd |||||
QY 1400 ACCTTTGCAAGAGTCAATCCAGCCATGTACATCCAGTGTTCCTCTGATGAACATCGCCA 1459
Dd |||||
QY 401 ThrPheAlaArgSerHisProAlaMetTyrAsnProValPheProMetAsnAsnArgPro 420
Dd |||||
QY 1460 ATAGTGATCAAAACGGATGTAATTTATCAATTTACAAATTTGCTGAGACCGAGTGGAT 1519
Dd |||||
QY 421 IleValIleLysThrAspValAsnTyrGlnPheThrGlnIleValValAspArgValAsp 440
Dd |||||
QY 1520 GGAGAAGTGGACATGATGTTATGTTTATCGAAGACAGATGTGGACCGTCTTAAA 1579
Dd |||||
QY 441 AlaGluAspGlyGlnTyrAspValMetPheIleGlyThrAspValGlyThrValLeuLys 460
Dd |||||
QY 1580 GTAGTTTCAATTCCTAAGGAGACTTGGTATGATTTAGAGAGTGTCTCTCGAAGAATG 1639
Dd |||||
QY 461 ValValSerIleProLysGluThrTrpTyrAspLeuGluValLeuLeuGluLysMet 480
Dd |||||
QY 1640 ACAGTTTTCGGAACCGAGTGTCTATTTTCAGAAATGGAGTTCCTCCTACAGCAGACAA 1699
Dd |||||
QY 481 ThrValPheArgGluProThrAlaIleSerAlaMetGluLeuSerThrLysGlnGlnGln 500
Dd |||||
QY 1700 CTATATATGTTTCAACGGTGGGTTCGCCAGTCCCTTTACACCGGTGTGATTTAC 1759
Dd |||||
QY 501 LeuTyrIleGlySerThrAlaGlyValAlaGlnLeuProLeuHisArgCysAspIleTyr 520
Dd |||||
QY 1760 GGGAAAGCGTGTGCTGAGTGTTCCTCGCCGAGACCCCTTACTGTGTGGATCGTCT 1819
Dd |||||
QY 521 GlyLysAlaCysAlaGluCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlySer 540
Dd |||||
QY 1820 GCATGTTCTCGTATTTTCCACTCGAAGAGACCCAGACAGCAGACAGATATAGAAAT 1879
Dd |||||
QY 541 AlaCysSerArgTyrPheProThrAlaLysArgArgThrArgGlnAspIleArgAsn 560
Dd |||||
QY 1880 GGAGACCCACTGACTGCTGTTTCCAGCTTACACCATGATATACCATGGCCACAGCCCT 1939
Dd |||||
QY 561 GlyAspProLeuThrHisCysSerAspLeuHisHisAspAsnHisHisGlyHisSerPro 580
Dd |||||
QY 1940 GAAGAGAGATCATCTATGTTGTAGATATAGTACACATTTTGGAAATGAGTCCCGAAG 1999
Dd |||||
QY 581 GluGluArgIleIleTyrGlyValGluAsnSerSerThrPheLeuGluCysSerProLys 600
Dd |||||
QY 2000 TCGCAGAGACCGCTGTCTATTGGCAATTCAGAGCGCAATTAAGAGCGGAAAGAGAG 2059
Dd |||||
QY 601 SerGlnArgAlaLeuValTyrTrpGlnPheGlnArgArgAsnGluGluArgLysGluGlu 620
Dd |||||
QY 2060 ATCAGAGTCCGATCATATCATCATCAGCAGATCAAGCGCTTCTCTAGTGTCTACAA 2119
Dd |||||
QY 621 IleArgValAspAspHisIleIleArgThrAspGlnGlyLeuLeuLeuArgSerLeuGln 640
Dd |||||
QY 2120 CAGAGGATTCAGGCAATTAACCTTCCATCGGTGGCAACATGGG 2164
Dd |||||
QY 641 GlnLysAspSerGlyAsnTyrLeuCysHisAlaValGluHisGly 655

US-09-946-374-310
Sequence 310, Application US/09946374
Publication No. US20030073129A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Fan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
FILE REFERENCE: P2830P1C1
CURRENT APPLICATION NUMBER: US/09/946,374
CURRENT FILING DATE: 2001-09-04
PRIOR APPLICATION NUMBER: 60/098716
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098723
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098749
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098750
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098803
PRIOR FILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/098821
PRIOR FILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/098843
PRIOR FILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/099536
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099596
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099598
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099602
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099642
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099741
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099754
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099763
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099792
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099808
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099812
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099815
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099816
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/100385
PRIOR FILING DATE: 1998-09-15
PRIOR APPLICATION NUMBER: 60/100388

;
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100390
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100584
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100627
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100661
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100662
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100664
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100683
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100684
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100710
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100711
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100848
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100849
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100919
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100930
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/101014
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101068
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101071
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101279
; PRIOR FILING DATE: 1998-09-22
; PRIOR APPLICATION NUMBER: 60/101471
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101472
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101474
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101475
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101476
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101477
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101479
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101738
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101741
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101743
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101915
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101916
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/102207
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102240
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102307
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102330
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102331
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102484
; PRIOR FILING DATE: 1998-09-30

;
; PRIOR APPLICATION NUMBER: 60/102487
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102570
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102571
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/102684
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102687
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/102965
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: 60/103258
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103314
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103315
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103328
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103395
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103396
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103401
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 60/103449
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103633
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103678
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103679
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103711
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/104257
; PRIOR FILING DATE: 1998-10-14
; PRIOR APPLICATION NUMBER: 60/104987
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105000
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105002
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105104
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/105169
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105266
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105693
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105694
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105807

Alignment Scores:
Pred. No.: 1.9e-201 Length: 777
Score: 2245.50 Matches: 413
Percent Similarity: 73.67% Conservative: 141
Best Local Similarity: 54.92% Mismatches: 177
Query Match: 45.86% Indels: 21
DB: 10 Gaps: 9

US-09-774-490-1 (1-2709) x US-09-946-374-310 (1-777)

QY 275 AAGAACATGTCACAGCTGAATATCTACAAAGAAATGTTGGAATCCAAATGTG 334
DB 39 LysGlnAsnIleProArgLeuLysLeuThrLysAspLeuLeuLeuSerAsnSerCys 58
QY 335 ATCACTTTCAATGGCTTGGCCACACAGCTCCAGTTATCATACCTTCCTTTGGATGAGAA 394
DB 59 IleProPheLeuGlySerSerGlyLeuAspPheGlnThrLeuLeuLeuAspGluGlu 78

US-10-206-915-348

Sequence 348, Application US/10206915
Publication No. US20040029221A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE OF INVENTION: ACIDS ENCODING THE SAME

FILE REFERENCES: P34301C153

CURRENT APPLICATION NUMBER: US/10/206,915

CURRENT FILING DATE: 2002-07-26

PRIOR APPLICATION NUMBER: 10/052586

PRIOR FILING DATE: 2002-01-15

PRIOR APPLICATION NUMBER: 60/059263

PRIOR FILING DATE: 1997-09-18

PRIOR APPLICATION NUMBER: 60/059266

PRIOR FILING DATE: 1997-09-18

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/063120

PRIOR FILING DATE: 1997-10-24

PRIOR APPLICATION NUMBER: 60/063121

PRIOR FILING DATE: 1997-10-24

PRIOR APPLICATION NUMBER: 60/063486

PRIOR FILING DATE: 1997-10-21

PRIOR APPLICATION NUMBER: 60/063540

PRIOR FILING DATE: 1997-10-28

PRIOR APPLICATION NUMBER: 60/063541

PRIOR FILING DATE: 1997-10-28

PRIOR APPLICATION NUMBER: 60/063544

PRIOR FILING DATE: 1997-10-28

Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 612

SEQ ID NO 348

LENGTH: 777

TYPE: PRT

ORGANISM: Homo Sapien

US-10-206-915-348

Alignment Scores:

Pred. No.:	1.9e-201	Length:	777
Score:	2245.50	Matches:	413
Percent Similarity:	73.67%	Conservative:	141
Best Local Similarity:	54.92%	Mismatches:	177
Query Match:	45.86%	Indels:	21
DB:	12	Gaps:	9

US-09-774-490-1 (1-2709) x US-10-206-915-348 (1-777)

QY	275	AAGAACATGTGCGCAGGCTGAATTCCTTCAAGAAATGTTGGAATCCACAACTGTG	334
DB	39	LysGlnAsnIleProArgLeuLysLeuThrTyrLysAspLeuLeuSerAsnSerCys	58
QY	335	ATCAGTTTCAATGGTGGCCACAGCTCCAGTTATCATACCTCTTTTGGATGAGAA	394
DB	59	IleProPheLeuGlySerSerGluGlyLeuAspPheGlnThrLeuLeuLeuAspGluGlu	78
QY	395	CGAGTAGCTGTATGTGGCAAGATCATATTTTCATTCGACCTGGTTAAATATC	454
DB	79	ArgGlyArgLeuLeuGlyAlaLysAspHisIlePheLeuLeuSerLeuValAspLeu	98
QY	455	---AAGGATTTTCAAAAGATTTGTGGCCAGATCTTACACCAAGAGAGATGAATGCAAG	511
DB	99	AsnLysAsnPheLysLysIleTyrTrpProAlaAlaLysGluArgValGluLeuLys	118

QY 1580 GTAGTTTCAATTCCTAAGGACCTTGATGATTAGAGAGGCTTCTGCTGGAAGAAATG 1639
 Db ValValserLysSerLysGluLysTrp--AsnMetGluValValLeuGluGluLeu 497
 QY 1640 ACAGTTTTCGGGACCGGACGCTGATTTACGCAATGAGGCTTCCACTAGAGCAACAA 1699
 Db GlnLeuPheLysHisSerLysIleLeuAsnMetGluLeuSerLeuLysGlnGlnGln 517
 QY 1700 CTATATATGTTTCAACCGGTGGGTTGCCAGCTCCCTTACACGGGTGATATTAC 1759
 Db LeuTyrlleGlySerArgAspGlyLeuValGlnLeuSerLeuHisArgCysAspThrTy 537
 QY 1760 GGGAAAGCTGTGCTGAGTGTGCTGCTGCGCCGAGACCTTACTGTGCTTGGATGCTCT 1819
 Db GlyLysAlaCysAlaAspCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlyAsn 557
 QY 1820 GCATGTTCTCGCTATTTTCCACTGCAAGAGAGCGACAGACCAAGATATAAGAAAT 1879
 Db AlaCysSerArgTyAlaProThrSerLysArgArgAlaArgGlnAspValLysTy 577
 QY 1880 GGACACCCAGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1939
 Db GlyAspProleThrGlnCysTrpAspIleLeuAspSerLysHisHis---GluThrAla 596
 QY 1940 CAACAGAGAAATCATCTATGCTGATAGAGATAGTAGCACATTTTGGAAATGCGAGT 1999
 Db AspGluLysValIlePheGlyIleGluPheAsnSerThrPheLeuGluCysIleProLys 616
 QY 2000 TCGCAGAGAGCTGGTGTCTATTGCAATTCAGAGCGGAAATGAAGAGCGAAAGAGAG 2059
 Db SerGlnGlnAlaThrIleLysTrpTyrlleGlnArgSerGlyAspGluHisArgGluGlu 636
 QY 2060 ATCAGAGTGGATGATATATCATCAGACAGATCAAGGCTTCTGCTAGTGTCTACAA 2119
 Db LeuLysProAspGluArgIleLysThrGluTyGlyLeuLeuIleArgSerLeuGln 656
 QY 2120 CAGAGAGTTCAGCAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2179
 Db LysLysAspSerGlyMetTyrlleCysLysAlaGlnGluHisThrPheIleHisThrIle 676
 QY 2180 CTTAAGGTACCTCGAAGTCATTCAGACAGACATTCGGAAGAACTTCTTCATTAAGAT 2239
 Db ValLysLeuThrLeuAsnValIleGluAsnGluLeuMetGluAsnThrGlnArgAlaGlu 696
 QY 2240 GATGATGAGAGGCTCTATAGCAACAAAGAAATGCTCAATAGCATACACCTAGCCAGAG 2299
 Db HisGluGluGlyGlnValLys-----AspLeuLeuAlaGluSerArg 710
 QY 2300 GTCTGCTACAGAGCTTCATGAGCTCATCAACACCCCACTTCACACGATGATGAG 2359
 Db LeuArgTyrlleLysAspTyrlleGlnIleLeuSerSerProAsnPhe---SerLeuAspGln 729
 QY 2360 TCTGCTGAAAGAGTTTGGAAAGAGGACCGGAAACAAACAGCTCGGCAAGGCCAGGACATACC 2419
 Db TyrCysGluGlnMetTrpHisArgGluLysArgGlnArgAsnLysGlyGly----- 747
 QY 2420 CCAGGAAACAGTAACTAAGTGAAGCACTTACAGAAATAAGAAAGGTAGAAAGAGGAGG 2479
 Db ProLysTrpLysHisMetGlnGluMetLysLysLysArgAsnArgArg 763
 QY 2480 ACCAC---GAATTTGAGAGGCGCCAGGAGTGTCT 2512
 Db HisHisArgAspLeuAspGluLeuProArgAlaVal 775

RESULT 8

US-10-199-670-348
 ; Sequence 348, Application US/10199670
 ; Publication No. US20040033560A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Chen, Jian
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Pan, James
 APPLICANT: Smith, Victoria
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 FILE REFERENCE: P3430R1C401
 CURRENT APPLICATION NUMBER: US/10/199,670
 CURRENT FILING DATE: 2002-07-19
 PRIOR APPLICATION NUMBER: 10/052586
 PRIOR FILING DATE: 2002-01-15
 PRIOR APPLICATION NUMBER: 60/059263
 PRIOR FILING DATE: 1997-09-18
 PRIOR APPLICATION NUMBER: 60/059266
 PRIOR FILING DATE: 1997-09-18
 PRIOR APPLICATION NUMBER: 60/062250
 PRIOR FILING DATE: 1997-10-17
 PRIOR APPLICATION NUMBER: 60/063120
 PRIOR FILING DATE: 1997-10-24
 PRIOR APPLICATION NUMBER: 60/063121
 PRIOR FILING DATE: 1997-10-24
 PRIOR APPLICATION NUMBER: 60/063486
 PRIOR FILING DATE: 1997-10-21
 PRIOR APPLICATION NUMBER: 60/063540
 PRIOR FILING DATE: 1997-10-28
 PRIOR APPLICATION NUMBER: 60/063541
 PRIOR FILING DATE: 1997-10-28
 PRIOR APPLICATION NUMBER: 60/063544
 PRIOR FILING DATE: 1997-10-28
 PRIOR APPLICATION data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 612
 SEQ ID NO 348
 LENGTH: 777
 TYPE: PRT
 ORGANISM: Homo Sapien
 US-10-199-670-348

Alignment Scores:
 Pred. No.: 1,9e-201 Length: 777
 Score: 2245.50 Matches: 413
 Percent Similarity: 73.67% Conservative: 141
 Best Local Similarity: 54.93% Mismatches: 177
 Query Match: 45.86% Indels: 21
 DB: 12 Gaps: 9

US-09-774-490-1 (1-2709) x US-10-199-670-348 (1-777)

QY 275 AAGACAAATGCTCCAGGCTGAATTTATCTTACAAAGAAATGTTGGATCCAAATGTG 334
 Db 39 LysGlnAsnIleProArgLeuLysLeuThrTyrlleAspLeuLeuSerAsnSerCys 58
 QY 335 ATCACTTTCAATGGCTTGCCCAACAGCTCCAGTTATCATACCTTCTCTTTGGATGAGAA 394
 Db 59 IleProPheLeuGlySerSerGluGlyLeuAspPheGlnThrLeuLeuAspGluGlu 78
 QY 395 CGGACTAGGCTGTATGTTGGAGCAAGGATCAGATATTTTTCATTCGACCTGGTTATATC 454
 Db 79 ArgGlyArgLeuLeuGlyAlaLysAspHisIlePheLeuLeuSerLeuValAspLeu 98
 QY 455 ---AAGGATTTTCAAAGATTTGCTGGCCAGTATCTTACACCAAGAGAGATGAATCAAG 511
 Db 99 AsnLysAsnPheLysIleTyrlleProAlaAlaLysGluArgValGluLeuLysLys 118
 QY 512 TCGGCTGGAAGACATCTCTGAAGATGCTCTAATTTTCATCAAGTACTTAAGGCATAT 571
 Db 119 LeuAlaGlyLysAspAlaAsnThrGluCysAlaAsnPheIleArgValLeuGlnProTyr 138
 QY 572 AATCACTCACTGTAGCTGTGGAGCGGGCTTTTTCATCAATTTTCACCTACATT 631
 Db 139 AsnLysThrHisIleTyrlleValCysGlyThrGlyAlaPheHisProIleCysGlyTyrlle 158


```

QY 1820 GCATGTTCTCGCTATTTCCCACTGCAAGAGAGCGCACAGACGACAAAGATATAGAAAT 1879
Db 558 AlcyserArgTyrAlaProThrSerLysArgAlaArgGlnAspValLysTyr 577
QY 1880 GGAGACCCACTGACTCTCTCTGAGACTTACACCATGATAATCACCATGCCACACGCCT 1939
Db 578 GlyAspProIleThrGlnCysTyrAspIleGluAspSerIleSerHis---GluThrAla 596
QY 1940 GAAGAGAGATCATCTATGTGTAGAGATATGAGACATTTTGGATTCGAGTCGAGAG 1999
Db 597 AspGluLysValIlePheGlyIleGluPheAsnSerThrPheLeuGluCysIleProLys 616
QY 2000 TCCAGAGACGCGTGTCTATTGGCAATTCACAGCGGAAATGAACAGCGAAAGAGAG 2059
Db 617 SerGlnGlnAlaThrIleLysTyrTyrIleGlnArgSerGlyAspGluHisArgGluGlu 636
QY 2060 ATCAGAGTGGATGATCATATCATCAGACAGATCAAGGCTCTGCTAGCTAGCTACAA 2119
Db 637 LeuLysProAspGluArgIleIleLysThrGluTyrGlyLeuLeuIleArgSerLeuGln 656
QY 2120 CAGAAGGATTCAGGCAATACCTCTGCCATGCGGTGGAACATGGGTTCATACAACTCTT 2179
Db 657 LysLysAspSerGlyMetTyrTyrCysLysAlaGlnGluHisThrPheIleHisThrIle 676
QY 2180 CTTAAGGTAACTCGGAAGTCAATGCACAGACAGCATTTGGAAGAACTTCTTCATAAAGAT 2239
Db 677 ValLysLeuThrLeuAsnValIleGluAsnGluGlnMetGluAsnThrGlnArgAlaGlu 696
QY 2240 GATGATGGAGTGGCTCTAAGACCAAGAAATGTCCAATAGCATGACACCTAGCCAGAG 2299
Db 697 HisGluGluGlyGlnValLys-----AspLeuLeuAlaGluSerArg 710
QY 2300 GTCTGTACAGAGACTTCATGCAAGTCTATCAACCCCAATCTCAACACGATGATGAG 2359
Db 711 LeuArgTyrLysAspTyrIleGlnIleLeuSerSerProAsnPhe---SerLeuAspGln 729
QY 2360 TTCTGTGACAAAGTTTGGAAAGGACCGAAACAACTGTCGCAAGGCCAGGACATACC 2419
Db 730 TyrCysGluGlnMetTyrHisArgGluLysArgGlnArgAsnLysGlyGly----- 747
QY 2420 CCAGGGAACAGTAACAAATGGAAGCACTTACAGAAATTAAGAAAGGTAGAACAGGAGG 2479
Db 748 -----ProLysTyrLysHisMetGlnGluMetLysLysLysArgAsnArgArg 763
QY 2480 ACCAC---GAATTTAGAGGGGACCCAGAGTGC 2512
Db 764 HisHisArgAspLeuAspGluLeuProArgAlaVal 775

RESULT 10
US-10-205-890-348
; Sequence 348, Application US/10205890
; Publication No. US20040048334A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P34301C519
; CURRENT APPLICATION NUMBER: US/10/205,890
; PRIOR FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18

```

```

; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 348
; LENGTH: 777
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-205-890-348

Alignment Scores:
Pred. No.: 1,9e-201 Length: 777
Score: 2245.50 Matches: 413
Percent Similarity: 73.67% Conservative: 141
Best Local Similarity: 54.92% Mismatches: 177
Query Match: 45.86% Indels: 21
DB: Gaps: 9

US-09-774-490-1 (1-2709) x US-10-205-890-348 (1-777)
QY 275 AAGAACAAATGTCCCAAGCTGAAATTTATCTCAAGAAATGTTGGAAATCAACAATGTG 334
Db 39 LysGlnAsnIleProArgLeuLysLeuThrTyrLysAspLeuLeuSerAsnSerCys 58
QY 335 ATCACTTTCAATGCTTGGCCAAACAGCTCCAGTTATCATCCTTCCCTTTGGATGAGAA 394
Db 59 IleProPheLeuGlySerSerGluGlyLeuAspPheGlnThrLeuLeuLeuAspGlu 78
QY 395 CGGAGTAGGCTGTATGTGGAGCAAGGATCACATATTTTCATTCGACCTGGTGAATATC 454
Db 79 ArgGlyArgLeuLeuLeuGlyAlaLysAspHisIlePheLeuLeuSerLeuValAspLeu 98
QY 455 ---AAGATTTTCAAAAGATTGTGCGCCAGTATCTTACACCAGAGAGAGTGAATGCAAG 511
Db 99 AsnLysAsnPheLysLysIleTyrTrpProAlaLysGluArgValGluLeuCysLys 118
QY 512 TGGCTGGAAGAACATCTCTGAAAGAAATGCTCAATTTTCATCAAGGTACTTAAGGCATAT 571
Db 119 LeuAlaGlyLysAspAlaAsnThrGluCysAlaAsnPheIleArgValLeuGlnProTyr 138
QY 572 AATCAGACTCATTGTACGCTGTGGAAACGGGGGCTTTTCATCAATTTGCACCTACATT 631
Db 139 AsnLysThrHisIleTyrValCysGlyThrGlyAlaPheHisProIleCysGlyTyrIle 158
QY 632 GAAATTGGACATCATCTGAGGACAAATATTTTAAAGTGGAGAACTCACATTTTGAAGAAC 691
Db 159 AspLeuGlyValTyrLysGluAspIleIlePheLysLeuAspThrHisAsnLeuGluSer 178
QY 692 GGGCGTGGGAAGAGTCCATATGACCCCTTAAGCTCTGACAGCATCCCTTTTAATAGATGA 751
Db 179 GlyArgLeuLysCysProPheAspProGlnGlnProPheAlaSerValMetThrAspGlu 198
QY 752 GAATTATCTCTGAACTCGAGCTGATTTTATCGGGCGAGACACTTCTATCTTCCCAACT 811
Db 199 TyrLeuTyrSerGlyThrAlaSerAspPheLeuGlyLysAspThrAlaPheThrArgSer 218
QY 812 CTTGGG-----CACCAACCAATCAGACAGAGAGCATGATCCAGGTGGCTC 862
Db 219 LeuGlyProThrHisAspHisHisTyrIleArgThrAspIleSerGluHisTyrTrpLeu 238

```


; PRIOR APPLICATION NUMBER: 60/063486
 ; PRIOR FILING DATE: 1997-10-21
 ; PRIOR APPLICATION NUMBER: 60/063540
 ; PRIOR FILING DATE: 1997-10-28
 ; PRIOR APPLICATION NUMBER: 60/063541
 ; PRIOR FILING DATE: 1997-10-28
 ; PRIOR APPLICATION NUMBER: 60/063544
 ; PRIOR FILING DATE: 1997-10-28
 ; Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 612
 ; SEQ ID NO 348
 ; LENGTH: 777
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 ; US-10-208-024-348

Alignment Scores:

Pred. No.: 1-9e-201 Length: 777
 Score: 2245.50 Matches: 413
 Percent Similarity: 73.67% Conservatives: 141
 Best Local Similarity: 54.92% Mismatches: 177
 Query Match: 45.86% Indels: 21
 DB: 12 Gaps: 9

US-09-774-490-1 (1-2709) x US-10-208-024-348 (1-777)

```

QY 275 AGAACAATGTCGAAGCTGAAATTTATCTTACAAAGAAATGTTGGAATCCAACTATG 334
DB 39 LysGlnAsnIleProArgLeuLysLeuThrTyrLysAspLeuLeuSerAsnSerCys 58
QY 335 ATCACTTTCAATGGCTGGCCACAGCTCCAGTATCATCATCTTCCTTTTGGATGAGAA 394
DB 59 IleProPheLeuGlySerSerGluGlyLeuAspPheGlnThrLeuLeuLeuAspGlu 78
QY 395 CGGAGTAGCTGTATGTTGGAGCAAGGATCATATTTTCAATTCAGCTGTTAATATC 454
DB 79 ArgGlyArgLeuLeuLeuGlyAlaLysAspHisIlePheLeuLeuSerLeuValAspLeu 98
QY 455 ---AAGATTTCAAAGATTGTTGGCCAGTATCTTACACAGAGAGATCAATGCAAG 511
DB 99 AsnLysAsnPhelLysIleTyrTrpProAlaLysGluArgValGluLeuLysCys 118
QY 512 TGGCTGGAAAAGACATCTGAAAGAAATGCTTAATTTTCATCAAGGTACTTAAGCATAT 571
DB 119 LeuAlaGlyLysAspAlaAsnThrGluCysAlaAsnPhelLeuArgValLeuGlnProTyr 138
QY 572 ATCACTGATCTGTACCCCTGTGGAACGGGGCTTTTCATCAATTTGCACTACATTT 631
DB 139 AsnLysThrHisIleTyrValCysGlyThrGlyAlaPheHisProIleCysGlyTyrIle 158
QY 632 GAAATGGACATCATCTCGAGCAACAATATTTTAAGCTGGAGAACTCATATTTGAAAC 691
DB 159 AspLeuGlyValTyrLysGluAspIleIlePheLysLeuAspThrHisAsnLeuGluSer 178
QY 692 GSCGTGGGAAGAGTCCATATGACCTTAAGCTGTCGACAGCATCCCTTTTAAATAGATGA 751
DB 179 GlyArgLeuLysCysProPheAspProGlnGlnProPheAlaSerValMetThrAspGlu 198
QY 752 GAATATATCTCGGAATCTCAGCTGATTTTATGGGGCGAGCTTTGCTATCTTCGAACT 811
DB 199 TyrLeuTyrSerGlyThrAlaSerAspPheLeuGlyLysAspThrAlaPheThrArgSer 218
QY 812 CTGGG-----CACCAACCAATCAGGACAGACAGCATGATTCAGGTGGCTC 862
DB 219 LeuGlyProThrHisAspHisIleTyrIleArgThrAspIleSerGluHisTyrTrpLeu 238
QY 863 ATGATCCAAAGTTCATATGTCGCCACCTCATCTCAGAGATGACAAATTCCTGAAGATGAC 922
DB 239 AsnGlyAlaLysPheIleGlyThrPhePheIleProAspThrTyrAsnProAspAsp 258
QY 923 AAAGTATATCTTTTCTCGTGAAATGCAATAGATGAGAACACTCTGGGAAAAGCTACT 982
DB 259 LysIleTyrPhePhePheArgGluSerSerGlnGluGlySerThrSerAspLysThrIle 278

```

```

QY 983 CACGCTAGATAGGTGCAGATATGCAAGATGACTTTGGAGGCGACAGAAAGTCTGGTGAAT 1042
DB 279 LeuSerArgValGlyArgValCysLysAsnAspValGlyGlyGlnArgSerLeuIleAsn 298
QY 1043 AAATGGACAACATTCCTCAAGCTCGTCTGATTTGCTCAGTGCCAGGTCCTCAATGGCAT 1102
DB 299 LysTrpThrThrPheLeuLysAlaArgLeuIleCysSerIleProGlySerAspGlyAla 318
QY 1103 GACACTCATTTTGTGACTCGAGATCTATTCCTAATGAACCTTAAAGATCCTTAAAT 1162
DB 319 AspThrTyrPheAspGluLeuGlnAspIleTyrLeuLeuProThrArgGluArgAsn 338
QY 1163 CCAGTTGTATATGGAGTGTTTTACGACTTCCAGTAACATTTTCAAGGATCAGCCGTGTGT 1222
DB 339 ProValValTyrGlyValPheThrThrSerSerIlePheLysGlySerAlaValCys 358
QY 1223 ATGTATAGCATGAGTATGTCAGAGAGGTGTTCTTGGTCCATATGCCCACAGGATGGA 1282
DB 359 ValTyrSerMetAlaAspIleArgAlaValPheAsnGlyProTyrAlaHisLysGluSer 378
QY 1283 CCCAACTATCAATGGTGCCTTATCAAGGAAGAGTCCCTTATCCAGCGCCAGGAACCTGT 1342
DB 379 AlaAspHisAsGTrpValGlnTyrAspGlyArgIleProTyrProArgProGlyThrCys 398
QY 1343 CCCAGCAAAACATTTTGTGTGT---TTGACTCTTACAAAGGACCTTCTCTGATGATGTTATA 1399
DB 399 ProSerLysThrTyrAspProLeuIleLysSerThrArgAspPheProAspAspValIle 418
QY 1400 ACCTTTCCAGAAGTCATCCAGCCATGACATCCAGTGTTCCTATGACAAATCGGCCA 1459
DB 419 SerPheLysArgHisSerValMetCysLysSerValTyrProValAlaGlyGlyPro 438
QY 1460 ATAGTGTCAATTCCTAAGGAGACTTGGTATGATTAGAAAGGTTCTCTGCGAAGAAATG 1519
DB 439 ThrPheLysArgIleAsnValAspTyrArgLeuThrGlnIleValValAspHisValIle 458
QY 1520 GCAGAGATCGACAGTATGATGTTATGTTATCGGAACAGATGTTGGACCGTCTTATAA 1579
DB 459 AlaGluAspGlyGlnTyrAspValMetPheLeuGlyThrAspIleGlyThrValLeuLys 478
QY 1580 GTAGTTTCAATTCCTAAGGAGACTTGGTATGATTAGAAAGGTTCTCTGCGAAGAAATG 1639
DB 479 ValValSerIleSerLysGluLysTrp---AsnMetGluValValLeuGluGluLeu 497
QY 1640 ACAGTTTTCGGGAACCGACTGCTATTTCAGCAATAGAGCTTCCACTAGCAGCAACAA 1699
DB 498 GlnIlePheLysHisSerSerIleLeuAsnMetGluLeuSerLeuLysGlnGln 517
QY 1700 CTATATATTGTTCAACGGCTGGGTTGCCAGCTCCCTTTACACCGGTGTGATATTAC 1759
DB 518 LeuTyrIleGlySerArgAspGlyLeuValGlnLeuSerLeuHisArgCysAspThrTyr 537
QY 1760 GGGAAACGCTGCTGAGTGTTCCTCGCCGAGACCTTACTGTGCTGGGATGTTCT 1819
DB 538 GlyLysAlaCysAlaAspCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlyAsn 557
QY 1820 GCATGTTCTCGCTATTTTCCACTGCAAGAGCGCACAGACGACAGATATAAGAAAT 1879
DB 558 AlaCysSerArgTyrAlaProThrSerLysArgAlaArgArgGlnAspValLysTyr 577
QY 1880 GGAGACCACTGACTGCTTCCAGATCTTACCATGATAATCACCATGGCCACAGCCCT 1939
DB 578 GlyAspProIleThrGlnCysTrpAspIleGluAspSerIleSerHis---GluThrAla 596
QY 1940 GAAGAGAGAAATCATATGTTGTTAGAGAAATAGTAGACATTTTGGAAATGCACTCCGAG 1999
DB 597 AspGluLysValIlePheGlyIleGluPheAsnSerThrPheLeuGluCysIleProLys 616
QY 2000 TCCAGAGAGCGCTGCTTATTCGCAATTCAGAGCGGAAATGCAAGCGGAAAGAGAG 2059
DB 617 SerGlnGlnAlaThrIleLysTrpTyrIleGlnArgSerGlyAspGluHisArgGluGlu 636

```


, PRIOR APPLICATION NUMBER: 60/065311
 , PRIOR FILING DATE: 1997-11-13
 , PRIOR APPLICATION NUMBER: 60/066120
 , PRIOR FILING DATE: 1997-11-21
 , PRIOR APPLICATION NUMBER: 60/066466
 , PRIOR FILING DATE: 1997-11-24
 , PRIOR APPLICATION NUMBER: 60/066772
 , PRIOR FILING DATE: 1997-11-24
 , PRIOR APPLICATION NUMBER: 60/069335
 , PRIOR FILING DATE: 1997-12-11
 , PRIOR APPLICATION NUMBER: 60/069425
 , PRIOR FILING DATE: 1997-12-12
 , PRIOR APPLICATION NUMBER: 60/069870
 , PRIOR FILING DATE: 1997-12-17
 , PRIOR APPLICATION NUMBER: 60/068017
 , PRIOR FILING DATE: 1997-12-18
 , PRIOR APPLICATION NUMBER: 60/077450
 , PRIOR FILING DATE: 1998-03-10
 , PRIOR APPLICATION NUMBER: 60/077632
 , PRIOR FILING DATE: 1998-03-11
 , PRIOR APPLICATION NUMBER: 60/077649
 , PRIOR FILING DATE: 1998-03-11
 , PRIOR APPLICATION NUMBER: 60/078886
 , PRIOR FILING DATE: 1998-03-20
 , PRIOR APPLICATION NUMBER: 60/078939
 , PRIOR FILING DATE: 1998-03-20
 , PRIOR APPLICATION NUMBER: 60/079664
 , PRIOR FILING DATE: 1998-03-27
 , PRIOR APPLICATION NUMBER: 60/079786
 , PRIOR FILING DATE: 1998-03-27
 , PRIOR APPLICATION NUMBER: 60/080107
 , PRIOR FILING DATE: 1998-03-31
 , PRIOR APPLICATION NUMBER: 60/080194
 , PRIOR FILING DATE: 1998-03-31
 , PRIOR APPLICATION NUMBER: 60/080327
 , PRIOR FILING DATE: 1998-04-01
 , PRIOR APPLICATION NUMBER: 60/080333
 , PRIOR FILING DATE: 1998-04-01
 , PRIOR APPLICATION NUMBER: 60/081049
 , PRIOR FILING DATE: 1998-04-08
 , PRIOR APPLICATION NUMBER: 60/081070
 , PRIOR FILING DATE: 1998-04-08
 , PRIOR APPLICATION NUMBER: 60/081195
 , PRIOR FILING DATE: 1998-04-09
 , PRIOR APPLICATION NUMBER: 60/081838
 , PRIOR FILING DATE: 1998-04-15
 , PRIOR APPLICATION NUMBER: 60/082568
 , PRIOR FILING DATE: 1998-04-21
 , PRIOR APPLICATION NUMBER: 60/082569
 , PRIOR FILING DATE: 1998-04-21
 , PRIOR APPLICATION NUMBER: 60/082704
 , PRIOR FILING DATE: 1998-04-22
 , PRIOR APPLICATION NUMBER: 60/082797
 , PRIOR FILING DATE: 1998-04-22
 , PRIOR APPLICATION NUMBER: 60/083322
 , PRIOR FILING DATE: 1998-04-28
 , PRIOR APPLICATION NUMBER: 60/083495
 , PRIOR FILING DATE: 1998-04-29
 , PRIOR APPLICATION NUMBER: 60/083496
 , PRIOR FILING DATE: 1998-04-29
 , PRIOR APPLICATION NUMBER: 60/083499
 , PRIOR FILING DATE: 1998-04-29
 , PRIOR APPLICATION NUMBER: 60/083559
 , PRIOR FILING DATE: 1998-04-29
 , PRIOR APPLICATION NUMBER: 60/084366
 , PRIOR FILING DATE: 1998-05-05
 , PRIOR APPLICATION NUMBER: 60/084414
 , PRIOR FILING DATE: 1998-05-06
 , PRIOR APPLICATION NUMBER: 60/084639
 , PRIOR FILING DATE: 1998-05-07
 , PRIOR APPLICATION NUMBER: 60/084640
 , PRIOR FILING DATE: 1998-05-07
 , PRIOR APPLICATION NUMBER: 60/084643

; PRIOR APPLICATION NUMBER: 60/089514
 ; PRIOR FILING DATE: 1998-06-16
 ; PRIOR APPLICATION NUMBER: 60/089538
 ; PRIOR FILING DATE: 1998-06-17
 ; PRIOR APPLICATION NUMBER: 60/089598
 ; PRIOR FILING DATE: 1998-06-17
 ; PRIOR APPLICATION NUMBER: 60/089653

Alignment Scores:
 Pred. No.: 1,9e-201 Length: 777
 Score: 2245.50 Matches: 413
 Percent Similarity: 73.67% Conservative: 141
 Best Local Similarity: 54.92% Mismatches: 177
 Query Match: 45.86% Indels: 21
 DB: 12 Gaps: 9

US-09-774-490-1 (1-2709) x US-10-174-581-348 (1-777)

QY	275	AGAGCAATGTCGCAAGCTGAATATCTCTACAAAGAAATGTTGAATCCCAATG	334
DB	39	LysGlnAsnIleProArgLeuLysLeuThrTyLysAspLeuLeuSerAsnSerCys	58
QY	335	ATCATTTCATCAATGGCTGGCCACAGCTCCAGTTATCATACCTCTCTTTGGATGAGAA	394
DB	59	IleProPheLeuGlySerSerGluGlyLeuAspPheGlnThrLeuLeuLeuAspGlu	78
QY	395	CGAGTAGCTGTATGTTGAGCAAGGATCATATTTTCATTCGACCTGGTTAATATC	454
DB	79	ArgGlyArgLeuLeuLeuGlyAlaLysAspHisIlePheLeuLeuSerLeuValAspLeu	98
QY	455	---AAGGATTTCAAAGATTGTTGGCCAGATCTTACACAGAGAGATGAATGCAG	511
DB	99	AsnLysAsnPheLysIleTyTrpProAlaAlaLysGluArgValGluLeuCysLys	118
QY	512	TGGCTGGGAAAGACATCTGAAAGAAATGTCTTAATTCATCAAGTACTTAAGCATAT	571
DB	119	LeuAlaGlyAspAlaAsnThrGluCysAlaAsnPheIleArgValLeuGlnProTy	138
QY	572	AATCAGATCACTGTACGCTGTGGAACGGGGCTTTTCATCCAAATTTGCACCTACAT	631
DB	139	AsnLysThrHisIleTyValCysGlyThrGlyAlaPheHisProIleCysGlyTyrlle	158
QY	632	GAAATGGACATCATCTCAGGACATATTTTAAAGCTGGAGACTCATCATTTTGAAGAC	691
DB	159	AspLeuGlyValTyrlsGluAspIleIlePheLysLeuAspThrHisAsnLeuGluSer	178
QY	692	GGCGTGGGAGAGTCCATACCTAAGCTGCTGACAGCATCCCTTTTAAATAGATGA	751
DB	179	GlyArgLeuLysCysProPheAspProGlnGlnProPheAlaSerValMetThrAspGlu	198
QY	752	GAATTATCTCGGAATCTGAGTATTTTATGGGGCGAGACTTTGCTATCTTCGGAAT	811
DB	199	TyrLeuTySerGlyThrAlaSerAspPheLeuGlyLysAspThrAlaPheThrArgSer	218
QY	812	CTTGGG-----CACCAACACCAATPACAGACAGACAGCATGATCCAGGTGGCTC	862
DB	219	LeuGlyProThrHisAspHisIleTyrlleArgThrAspIleSerGluHisTyrlleu	238
QY	863	AATGATCCAAAGTTCAATTAGTCCCACTCTCTCAGAGAGTGAACAATCTCGAATGAC	922
DB	239	AsnGlyAlaLysPheIleGlyThrPhePheIleProAspThrTyrlleAsnProAspAsp	258
QY	923	AAAGTATCTTTCTTCGTTGCAATGCAATGATGAGACACTCTCGGAAGAGCTACT	982
DB	259	LysIleTyPhePhePheArgGluSerGlnGluGlySerThrSerAspLysThrile	278
QY	983	CACGTAGAAATAGTTCAGATATGCAAGATGACTTTTGGAGGGCACAGAGTCTGGTGAAT	1042
DB	279	LeuSerArgValCylArgValCysLysAsnAspValGlyGlyGlnArgSerLeuIleAsn	298
QY	1043	AAATGACACATCTCTCAAGCTCTGCTGATTCTCTCAGTCCGAGGTCCAAATGGCAT	1102
DB	299	LysTrpThrPheLeuLysAlaArgLeuIleCysSerIleProGlySerAspGlyAla	318

QY	1103	GACACTCATTTTGTATGAATGAACTGAGATATTCCTTAATGAATCTTAAAGATCTTAA	1162
DB	319	AspThrTyPheAspGluLeuGlnAspIleTyrlleLeuLeuProThrArgAspGluArgAsn	338
QY	1163	CCAGTTGTATATGGAGTGTTCACGACTTCCAGTACATATTTTCAAGGGATACCGCTGT	1222
DB	339	ProValValTyGlyValPheThrThrSerSerIlePheLysGlySerAlaValCys	358
QY	1223	ATGTATACATGATGATGTCAGAGGGTGTTCCTTGTCTCATATGCCACAGGATGGA	1282
DB	359	ValTySerMetAlaAspIleArgAlaValPheAsnGlyProTyAlaHisLysGluSer	378
QY	1283	CCCAACTATCAATGGTGCCTTATCAAGAAAGATCCCTATCCACGGCCAGGAACTTGT	1342
DB	379	AlaAspHisArgTrpValGlnTyAspGlyArgIleProTyProArgProGlyThrCys	398
QY	1343	CCCAGCAAAACATTTGGTGGT---TTTGACTCTCAAAAGGACCTCTCTGATGATGTTATA	1399
DB	399	ProSerLysThrTyAspProLeuIleLysSerThrArgAspPheProAspAspValle	418
QY	1400	ACCTTTGCAAGAAGTATCCAGCCATGATACATCCAGTGTTCCTATGAAACAATCGGCCA	1459
DB	419	SerPheIleLysArgHisSerValMetTyrlsSerValTyrlsProValAlaGlyGlyPro	438
QY	1460	ATAGTGATCAAAACCGATGTAATTTATCAATTTACAAATTTGCTAGACCGAGTGGAT	1519
DB	439	ThrPheLysArgIleAsnValAspTyArgLeuThrGlnIleValAlaAspHisValle	458
QY	1520	GCAGAGATGACATGATGTTATGTTATTCGAAACAGATGTTGGACCGTCTTCTTAAA	1579
DB	459	AlaGluAspGlyGlnTyAspValMetPheLeuGlyThrAspIleGlyThrValleuLys	478
QY	1580	GTAGTTCAATTCCTAAGGACATTTGATGATTTTACAAGAGGTTCTGCTGGAAGAATG	1639
DB	479	ValValSerIleSerLysGluLysTrp---AsnMetGluGluValValLeuGluGluLeu	497
QY	1640	ACAGTTTTCGGGAACCGCATGCTTATTTTCAGCAATGAGCTTTTCCACTAAGCAGCAACA	1699
DB	498	GlnIlePheLysHisSerSerIleLeuAsnMetGluLeuSerLeuLysGlnGlnGln	517
QY	1700	CTATATATTTGGTTCAACGGCTGGGTGGCTCCAGTCTCTTACACCGGTGTGATATTAC	1759
DB	518	LeuTyrlleGlySerArgAspGlyLeuValGluLeuSerLeuHisArgCysAspThrTy	537
QY	1760	GGGAAAGCGTGTGCTGAGTGTGCTCGCCGAGACCTTACTGTCTGCTGGGATGGTCT	1819
DB	538	GlyLysAlaCysAlaAspCysLeuAlaArgAspProTyCysAlaIlePheAspGlyAsn	557
QY	1820	GCATGTTCTCGCTATTTTCCACTGCAAGAGACGCAAGACAGCAAGATATAAGAAAT	1879
DB	558	AlaCysSerArgTyAlaProThrSerLysArgAlaArgAlaArgGlnAspValLysTy	577
QY	1880	GGAGACCCACTGACTCTCTTCCAGCTTACACCATGATATCCCATGCGCCACGCCCT	1939
DB	578	GlyAspProIleThrGlnCysTrpAspIleGluAspSerIleSerHis---GluThrAla	596
QY	1940	GAAGAGAAATCATCTATGTTAGAGATATGATGACACATTTTGGAAATGCAGTCCGAAG	1999
DB	597	AspGluLysValIlePheGlyIleGluPheAsnSerThrPheLeuGluCysIleProLys	616
QY	2000	TCCAGAGAGCGGTGCTTATGCGAATTCACAGGGGAAATGAAGCGCAAGAGAGAG	2059
DB	617	SerGlnGlnAlaThrIleLysTrpTyrlleGlnArgSerGlyAspGluHisArgGluGlu	636
QY	2060	ATCAGATGATCATATCATCATGACAGATCAAGGCGCTCTGCTACGTCTGTACAA	2119
DB	637	LeuLysProAspGluArgIleIleLysThrGluTyGlyLeuLeuIleArgSerLeuGln	656
QY	2120	CAGAGATTTCAGCAATTTACTCTCTGCGATCGCGTGAACATGGGTTCATACAACTCT	2179
DB	657	LysLysAspSerGlyMetTyrlTyCysLysAlaGlnGluHisThrPheIleHisThrile	676


```

1520 GCAGAGATGCGACGATGATGTTATGTTTATCGGAACACAGATGTTGGGACCGCTCTTAA 1579
Db AlaGluAspGlyGlnThrAspValMetPheLeuGlyThrAspIleGlyThrValLeuLys 478
1580 GTAGTTTCAATCTTAAGAGAGACTGGTATGATTTAGAAAGAGTCTGCTGCGAAGATG 1639
Db ValValSerIleSerLysGlyLysTrp---AsnMetGluGluValValLeuGluGluLeu 497
1640 ACAATTTTTCGGGAACCGACTGCTATTTTCAGCAATGGAGCTTTCCACTAAGCAGCAACA 1699
Db GlnIlePheLysHisSerSerIleLeuLeuAsnMetGluLeuSerLeuLysGlnGln 517
1700 CTATATATGTTTCAACGGCTGGGTTGCCAGCTCCCTTTACCGGTGTGATATTAC 1759
Db LeuTyIleGlySerArgAspGlyLeuValGlnLeuSerLeuHisArgCysAspThrTy 537
1760 GGAAGAGCTGCTGAGTGGTCCCTCGCCCGAGACCTTACTGCTGGATGGATGCT 1819
Db GlyLysAlaCysAlaAspCysCysLeuAlaArgAspProTyCysAlaTrpAspGlyAsn 557
1820 GCATGTTCTCGCTATTTCCCACTGCAAGAGACGCAAGACGCAAGACATATAAGAAAT 1879
Db AlaCysSerArgTyAlaProThrSerLysArgAlaArgArgGlnAspValLysTy 577
1880 GGAGACCCACTGACTGCTGCTGCTACACCTTACACCATGATATCACCATGGCCACAGCCCT 1939
Db GlyAspProIleThrGlnCysTrpAspIleGluAspSerIleSerHis---GluThrAla 596
1940 GAAGAGAGATCATCTATGCTGTAGAGATAGTAGACATTTTGGATGAGTCCGAG 1999
Db AspGluLysValIlePheGlyIleGluPheAsnSerThrPheLeuGluCysIleProLys 616
2000 TGCAGAGAGCGCTGCTTATTTGGCAATTCAGAGCGGCAATGAAGAGCGAAAGAGAG 2059
Db SerGlnGlnAlaThrIleLysTrpTyIleGlnArgSerGlyAspGluHisArgGlu 636
2060 ATCAGAGTGGATGATCATATCATCAGACAGATCAAGGCTTCTGCTAGTGTCTACAA 2119
Db LeuLysProAspGluArgIleIleLysThrGlyTyGlyLeuLeuIleArgSerLeuGln 656
2120 CAGAGAGATTCAGGCAATTTACCTCTGCCATGGGTGGACATGGGTTTCATCAAACTCT 2179
Db LysLysAspSerGlyMetTyTyTyCysLysAlaGlnGluHisThrPheIleHisThrIle 676
2180 CTTAAGTTAACCTGGAAGTCTATGACAGAGCATTTGGAGAACTTCTTCATAAAGAT 2239
Db ValLysLeuThrLeuAsnValIleGluAsnGluGlnMetGluAsnThrGlnArgAlaGlu 696
2240 GATGATGGAGATGGCTCTTAAGACCAAGAAATGTCCAATAGCATCACACCTAGCCAGAG 2299
Db HisGluGluGlyGlnValLys-----AspLeuLeuAlaGluSerArg 710
2300 GTCTGTGATCAGAGACTTCATGAGCTATCAACACCCCAATCTCAACACGATGATGAG 2359
Db LeuArgTyLysAspTyIleGlnIleLeuSerSerProAsnPhe---SerLeuAspGln 729
2360 TTCTGTGAACAAGTTTGGAAAGGACCGAACAACCTGCGCAAGGCCGAGCATACC 2419
Db TyCysGluGlnMetTrpHisArgGluLysArgGlnArgGlnArgGlnGlyGly----- 747
2420 CCAGGGAACAGTAACAATGGAAGCACTTACAGAAATAAGAAAGGTAGAAACAGGAGG 2479
Db ProlLysTrpLysHisMetGlnGluMetLysLysLysLysLysLysLysLysLysLys 763
2480 ACCAC---GAATTCAGAGGCGACCCAGGATGTC 2512
Db HisHisArgAspLeuAspGluLeuProArgAlaVal 775

```

RESULT 15

US-10-176-749-348

; Sequence 348, Application US/10176749

; Publication No. US20030017542A1

```

; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C76
; CURRENT APPLICATION NUMBER: US/10/176,749
; CURRENT FILING DATE: 2002-06-20
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 348
; LENGTH: 777
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-749-348

```

```

Alignment Scores:
Pred. No.: 1,9e-201
Score: 2245.50
Percent Similarity: 73.67%
Best Local Similarity: 54.92%
Query Match: 45.86%
DB: 12
Length: 777
Matches: 413
Conservative: 141
Mismatches: 177
Indels: 21
Gaps: 9

```

```

US-09-774-490-1 (1-2709) x US-10-176-749-348 (1-777)
Qy 275 AAGAACAAATGTGCCAAGCTGAAATATCTCAACAAAGAAATGTTGGAATCAACAATGTG 334
Db 39 LysGlnAsnIleProArgLeuLysLeuThrTyLysAspLeuLeuSerAsnSerCys 58
Qy 335 ATCACTTTCAATGGCTTGGCCAAACAGCTCCAGTTATCATACCTTCCTTTTGGATGAGAA 394
Db 59 IleProPheLeuGlySerSerGluGlyLeuAspPheGlnThrLeuLeuLeuAspGlu 78
Qy 395 CGAGTAGGCTGTATGTGGAGCAAGGATCACAATTTTCATCGACCTGGTTAATATC 454
Db 79 ArgGlyArgLeuLeuLeuGlyAlaLysAspHisIlePheLeuLeuSerLeuValAspLeu 98
Qy 455 ---AAGATTTCCTCAAAAGATTGTGTGCCAGTATCTTACACCAAGAGAGATGAATGCAAG 511
Db 99 AsnLysAsnPheLysLysIleTyTrpProAlaAlaLysGluArgValGluLeuCysLys 118
Qy 512 TGGCTGGAAAGACATCTCTGAAAGATGTGCTTAATTCATCAAGGTACTTAAGGCATAT 571
Db 119 LeuAlaGlyLysAspAlaAsnThrGluCysAlaAsnPheIleArgValLeuGlnProTy 138
Qy 572 AATCAGACTCACCTGTACGCTGTGAAACGGGGCTTTTCATCCAAATTTGCACCTACAT 631
Db 139 AsnLysThrHisIleTyValCysGlyThrGlyAlaPheHisProIleCysGlyTyIle 158
Qy 632 GAAATTGGAATCATCTCTGAGACATATTTTAACTGGAGAACTCACATTTTGAAGAAC 691
Db 159 AspLeuGlyValTyLysGluAspIleIlePheLysLeuAspThrHisAsnLeuGluSer 178
Qy 692 GGGCTGGGAAGAGTCCATATGACCTTAAGCTCTGACAGCATCCCTTTTAAATAGATGA 751
Db 179 GlyArgLeuLysCysProPheAspProGlnGlnProPheAlaSerValMetThrAspGlu 198
Qy 752 GAATTATCTCTGAACTGCAGCTGATTTTATGGGCGAGACTTTGCTATCTTCCGAAC 811
Db 199 TyLeuTySerGlyThrAlaSerAspPheLeuGlyLysAspThrAlaPheThrArgSer 218
Qy 812 CTTGGG-----CACACCAACCAATCAGACAGAGCAGCATGATTCAGGTGGCTC 862

```

Db 219 LeuGlyProThrHisAspHisHisTyrIleArgThrAspIleSerGluHisTyrTrpLeu 238
 QY 863 AATGATCCAAAGTTCAATAGTGGCCACCTCATCTCAGAGAGTACAAATCCTCAAGATGAC 922
 Db 239 AsnGlyAlaLysPheIleGlyThrPhePheIleProAspThrTyrAsnProAspAsp 258
 QY 923 AAAGTATACATTTCTTCCTGAAATGCAATAGATGGAGAACACTCTCGAAAGCTACT 982
 Db 259 LysIleTyrPhePheAspGlySerSerGlnGluGlySerThrSerAspLysThrIle 278
 QY 983 CACCTAGATAGTTCAGATATCAGAAATGATTTGGAGGCGACAGAGTGTGTGAT 1042
 Db 279 LeuSerArgValGlyArgValCysLysAsnAspValGlyGlyLysSerLeuIleAsn 298
 QY 1043 AAATGGACAACTTCCTCAAGCTCGTCTGATTGCTCAGTCCAGGTCCTCAATGGCATT 1102
 Db 299 LysTrpThrThrPheLeuLysAlaArgLeuIleCysSerIleProGlySerAspGlyAla 318
 QY 1103 GACACTCATTTGATGACTGCAGGATGATTCCTTAATGAATCTTAAAGATCCTAAAT 1162
 Db 319 AspThrTyrPheAspGluLeuGlnAspIleTyrLeuLeuProThrArgAspGluArgAsn 338
 QY 1163 CCAGTTGATATGAGTGTTCAGCTTCAGTAACATTTTCAAGGGATCAGCCGTGTGT 1222
 Db 339 ProValValTyrGlyValPheThrThrThrSerSerIlePheLysGlySerAlaValCys 358
 QY 1223 ATGTATAGCATGATGATGAGAGGGTTCCTTGTTCCTATATGCTCCACAGGGATGGA 1282
 Db 359 ValTyrSerMetAlaAspIleArgAlaValPheAsnGlyProTyrAlaHisLysGluSer 378
 QY 1283 CCCAACTATCAATGGTGTTCCTATCAAGAAAGATGCCCTATCCACGGCCAGGAATGT 1342
 Db 379 AlaAspHisArgTrpValGlnTyrAspGlyArgIleProTyrProArgProGlyThrCys 398
 QY 1343 CCCAGCAAAACATTTGGTGTGTTTGACTCTCAAGAGGACCTTCCTGATGATGTATATA 1399
 Db 399 ProSerLysThrTyrAspProLeuIleLysSerThrArgAspPheProAspValIle 418
 QY 1400 ACCTTTTCCAAAGATCATCCAGCCATGATCAATCCAGTGTTCCTATCAACAAATCGCCA 1459
 Db 419 SerPheIleLysArgHisSerValMetTyrLysSerValTyrProValAlaGlyGlyPro 438
 QY 1460 ATAGTATCAAAACGATGATTAATATCAATTTACAAATTTGCTGTAGACCGGATGAT 1519
 Db 439 ThrPheLysArgIleAsnValAspTyrArgLeuThrGlnIleValValAspHisValIle 458
 QY 1520 GCAGAGATGCAGATGATGATTTATGTTATCGGAACAGATGTTGGACCGTCTCTTAAA 1579
 Db 459 AlaGluAspGlyGlnTyrAspValMetPheLeuGlyThrAspIleGlyThrValLeuLys 478
 QY 1580 GTAGTTTCAATTCCTAAGAGACTGGTATGATTTAGAGAGGTCTCTCTGGAGAAATG 1639
 Db 479 ValValSerIleSerLysGluLysTrp---AsnMetGluGluValValLeuGluGluLeu 497
 QY 1640 ACAGTTTTCGGGAACCGACTGCTATTTCAGCAATGGAGCTTCCACTTAAGCAGCAACA 1699
 Db 498 GlnIlePheLysHisSerSerIleLeuLeuAsnMetGluLeuSerLeuLysGlnGlnGln 517
 QY 1700 CTATATATGGTTCAACGGCTGGGTGGCCAGCTCCCTTTACACCGGTGTGATTTAC 1759
 Db 518 LeuTyrIleGlySerArgAspGlyLeuValGlnLeuSerLeuHisArgCysAspThrTyr 537
 QY 1760 GGGAAAGCGTGTCTGATGTTGCTTCGCGCCGAGACCTTACTGTCTTGGATGGTCT 1819
 Db 538 GlyLysAlaCysAlaAspCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlyAsn 557
 QY 1820 GCAATGTTCTCGCTATTTTCCCACTGCAAGAGACCGCACAGACGACAGATATTAAGAAAT 1879
 Db 558 AlaCysSerArgTyrAlaProThrSerLysArgAlaArgArgGlnAspValLysTyr 577
 QY 1880 GGAGACCCACTGACTCAGCTGTTTCAGACTTACACCATGATTAATCCATGCGCCACAGCCCT 1939
 Db 578 GlyAspProIleThrGlnCysTrpAspIleGluAspSerIleSerHis---GluThrAla 596

QY 1940 GAAGAGAGAAATCATCTATGCTGTAGAGAAATAGTACACATTTTGGAAATGCGATCCGAAG 1999
 Db 597 AspGluLysValIlePheGlyIleGluPheAsnSerThrPheLeuGluCysIleProLys 616
 QY 2000 TCCAGAGAGCGCTCGTCTATTGGCAATTCAGAGCGCGAAATGAAGAGCGGAAAGAGAG 2059
 Db 617 SerGlnGlnAlaThrIleLysTrpTyrIleGlnArgSerGlyAspGluHisArgGluGlu 636
 QY 2060 ATCAGAGTGCATCATCATATCATCAGACAGATCAAGCGCTTCTGCTACGTAGTCTACAA 2119
 Db 637 LeuLysProAspGluArgIleIleLysThrGluTyrGlyLeuLeuIleArgSerLeuGln 656
 QY 2120 CAGAGAGATTACGGCAATTAATCCTCTGCTCGGTTGGAAACATGGGTTTCATACAAACTCTT 2179
 Db 657 LysLysAspSerGlyMetTyrTyrCysLysAlaGlnGluHisThrPheIleHisThrIle 676
 QY 2180 CTTAAGGTAAACCTCGAAGTCAATTCACACAGAGCATTTGGAGAACTTCTTCATAAAGAT 2239
 Db 677 ValLysLeuThrLeuAsnValIleGluAsnGluGlnMetGluAsnThrGlnArgAlaGlu 696
 QY 2240 GATGATGGAGATGGCTCTTAAGCAAGAAATGTCCAATAGCATGACACCTTAGCCAGAAG 2299
 Db 697 HisGluGluGlyGlnValLys-----AspLeuLeuAlaGluSerArg 710
 QY 2300 GTCTGGTACAGAGATTTTCATGCGCTCATCAACACCCCATCTCAACAGATGATGAG 2359
 Db 711 LeuArgTyrLysAspIleGlnIleLeuSerSerProAsnPhe---SerLeuAspGln 729
 QY 2360 TTCTGTGAAACAGTTTGGAAAGGCGACCGAAACAAACGTCGGCAAGCCGAGGACATACC 2419
 Db 730 TyrCysGluGlnMetTrpHisArgGluLysArgArgGlnArgAsnLysGlyGly----- 747
 QY 2420 CCAGGGAACAGTAACAAATGGAGCACTTACAGAAATAGAAAGGTAGAAACAGAGG 2479
 Db 748 -----ProLysTrpLysHisMetGlnGluMetLysLysLysArgAsnArgArg 763
 QY 2480 ACCCAC---GAATTTGAGAGGGCGACCCAGGAGTGTCT 2512
 Db 764 HisHisArgAspLeuAspGluLeuProArgAlaVal 775

Search completed: September 21, 2004, 20:34:16
 Job time : 398 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: September 21, 2004, 19:36:33 ; Search time 53.5 Seconds
(without alignments)
5229.215 Million cell updates/sec

Title: US-09-774-490-1

Perfect score: 4896

Sequence: 1 aatctttttttatgatg.....aggctttttttcttaacc 2709

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 778928

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p.model -DEV=xlp
-O=/cgn2_1/USGTO.spool.p/US09774490/runat_21092004.144246.2377/app.query.fasta_1.2887
-DB=Issued Patents AA -QEXT=fastan -SUFFIX=rai -MINMATCH=0.1 -LOOFCLO=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09774490@cgn.1.1.74 @runat_21092004.144246.2377 -NCPUS=6 -ICPU=3
-NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents AA:*
1: /cgn2_6/prodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/prodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/prodata/2/iaa/5A_COMB.pep.*
4: /cgn2_6/prodata/2/iaa/5B_COMB.pep.*
5: /cgn2_6/prodata/2/iaa/5A_COMB.pep.*
6: /cgn2_6/prodata/2/iaa/5B_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4201	85.8	771	1	US-08-121-713D-54
2	4201	85.8	771	1	US-08-835-268-54
3	4201	85.8	771	2	US-09-060-692-54
4	4201	85.8	771	3	US-08-833-391-54
5	4201	85.8	771	4	US-09-060-610-54
6	4201	85.8	771	5	PCT-US94-10151A-54
7	3568	72.9	655	4	US-08-556-422A-3
8	2562	52.3	477	1	US-08-136-922-2
9	2030	41.5	775	4	US-09-308-179B-1
10	982.5	20.1	862	4	US-08-556-422A-2
11	838.5	17.1	607	4	US-08-556-422A-4
12	817	16.7	1070	4	US-09-653-274-8

13	817	16.7	1086	4	US-09-653-274-4	Sequence 4, Appli
14	816.5	16.7	641	4	US-09-653-274-13	Sequence 13, Appl
15	785.5	16.0	724	1	US-08-121-713D-62	Sequence 62, Appl
16	785.5	16.0	724	1	US-08-835-268-62	Sequence 62, Appl
17	785.5	16.0	724	2	US-09-060-692-62	Sequence 62, Appl
18	785.5	16.0	724	3	US-08-833-391-62	Sequence 62, Appl
19	785.5	16.0	724	4	US-09-060-610-62	Sequence 62, Appl
20	785.5	16.0	724	5	PCT-US94-10151A-62	Sequence 62, Appl
21	785.5	15.6	536	4	US-09-653-274-10	Sequence 10, Appl
22	765.5	15.6	930	4	US-09-254-594-6	Sequence 6, Appl
23	762.5	15.6	730	1	US-08-121-713D-58	Sequence 58, Appl
24	762.5	15.6	730	1	US-08-835-268-58	Sequence 58, Appl
25	762.5	15.6	730	2	US-09-060-692-58	Sequence 58, Appl
26	762.5	15.6	730	3	US-08-833-391-58	Sequence 58, Appl
27	762.5	15.6	730	4	US-09-060-610-58	Sequence 58, Appl
28	762.5	15.6	730	5	PCT-US94-10151A-58	Sequence 58, Appl
29	738.5	15.1	650	1	US-08-121-713D-60	Sequence 60, Appl
30	738.5	15.1	650	1	US-08-835-268-60	Sequence 60, Appl
31	738.5	15.1	650	2	US-09-060-692-60	Sequence 60, Appl
32	738.5	15.1	650	3	US-08-833-391-60	Sequence 60, Appl
33	738.5	15.1	650	4	US-09-060-610-60	Sequence 60, Appl
34	738.5	15.1	650	5	PCT-US94-10151A-60	Sequence 60, Appl
35	723.5	14.8	929	4	US-09-254-594-3	Sequence 3, Appli
36	723	14.8	887	4	US-09-077-940A-2	Sequence 2, Appli
37	718	14.7	425	4	US-08-556-422A-7	Sequence 7, Appli
38	712.5	14.6	888	4	US-09-077-940A-4	Sequence 4, Appli
39	680	13.9	712	1	US-08-121-713D-64	Sequence 64, Appl
40	680	13.9	712	1	US-08-835-268-64	Sequence 64, Appl
41	680	13.9	712	2	US-09-060-692-64	Sequence 64, Appl
42	680	13.9	712	3	US-08-833-391-64	Sequence 64, Appl
43	680	13.9	712	4	US-09-060-610-64	Sequence 64, Appl
44	680	13.9	712	5	PCT-US94-10151A-64	Sequence 64, Appl
45	654.5	13.4	666	3	US-09-240-410-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-121-713D-54
; Sequence 54, Application US/08121713D
; Patent No. 5639856
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey S.
; APPLICANT: Kolodkin, Alex L.
; APPLICANT: Matthes, David
; APPLICANT: Bentley, David R.
; APPLICANT: O'Connor, Timothy
; TITLE OF INVENTION: The Semaphorin Gene Family
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 Bush Street, Suite 3200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/121,713D
; FILING DATE: 13-SEP-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A.
; REGISTRATION NUMBER: 36, 627
; REFERENCE/DOCKET NUMBER: B94-002-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; TELEX:

; INFORMATION FOR SEQ ID NO: 54:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 771 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-121-713D-54

Alignment Scores:

Pred. No.: 0
 Score: 4201.00
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 85.80%
 DB: 1

US-09-774-490-1 (1-2709) x US-08-121-713D-54 (1-771)

QY	200	ATGGCTGGTTAACTAGGATGTGCTGCTTTCTGGGGAGTATTACTTACAGCAAGACA	259
DB	1	MetGlyTrpLeuThrArgIleValCysLeuPheTrpGlyValLeuLeuThrAlaArgAla	20
QY	260	AACATCAGATGGAGAGACAATGTGCCAAGCTGAATTTATCTTACAAAGAAATGTG	319
DB	21	AsnTyrGlnAsnGlyLysAsnAsnValProArgLeuLysLeuSerTyrLysGluMetLeu	40
QY	320	GAATCCCAACATGTGATCACTTTCAATGGCTTCCGCAACAGCTCCAGTTTATCATACCTTC	379
DB	41	GlusSerAsnValIleThrPheAsnGlyLeuAlaAsnSerSerTyrHisThrPhe	60
QY	380	CTTTTGATGAGAACGGAGTAGCTGTATGTGGAGCAAGAGATCAATATTTTCATTC	439
DB	61	LeuLeuAspGluCysArgSerArgLeuTyrValGlyAlaLysAspHisIlePheSerPhe	80
QY	440	GACCTGTTTAATATCAAGGATTTTCAAAAGATTGTGTGCCAGTATCTTACACCAAGA	499
DB	81	AspLeuValAsnIleLysAspPheGlnLysIleValTrpProValSerTyrThrArg	100
QY	500	GATGAATGCAAGTGGCTGAAAGACATCTGAAAGATGTGCTAAATTCATGAAGTA	559
DB	101	AspGluCysLysTrpAlaGlyLysAspIleLeuLysGluCysAlaAsnPheIleLysVal	120
QY	560	CTTAAGGCATATATCAGACTCACTTGATCGCTGTGGAACGGGGCTTTTCATCCAAT	619
DB	121	LeuLysAlaTyrAsnGlnThrHisLeuTyrAlaCysGlyThrGlyAlaPheHisProIle	140
QY	620	TGCACCTACATTTGAATTTGACATCATCTGAGGACAAATATTTTAAGCTGGAGACTCA	679
DB	141	CysThrTyrIleGluIleGlyHisHisProGluAspAsnIlePheLysLeuGluAsnSer	160
QY	680	CATTTTGAAACCGCTGGGAAGAGTCCATATGACCTTAAGCTGTGACAGCATCCCTT	739
DB	161	HisPheGluAsnGlyArgGlyLysSerProTyrAspProLysLeuLeuThrAlaSerLeu	180
QY	740	TTAATAGATGGAATTTACTCTGGAATCTGAGCTGATTTTATGGCGGAGACTTTCCT	799
DB	181	LeuIleAspGlyLeuLeuTyrSerGlyThrAlaAlaAspPheMetGlyArgAspPheAla	200
QY	800	ATCTTCGGAATCTTGGGCACACCAACCAATCAGACAGACAGACATGATTCAGAGTGG	859
DB	201	IlePheArgThrLeuGlyHisHisHisProIleArgThrGluGlnHisAspSerArgTrp	220
QY	860	CTCAATGATCCAAAGTTTCAATAGTCCCACTCATCTCAGAGATGACAAATCTCTGAAGAT	919
DB	221	LeuAsnAspProLysPheIleSerAlaHisLeuIleSerGluSerAspAsnProGluAsp	240
QY	920	GACAAAGTATACATTTTCTTCGCTGAAATGCAATAGATGGAGAACACTCTGGAAAGCT	979
DB	241	AspLysValTyrPhePheArgGluAsnAlaIleAspGlyGluHisSerGlyLysAla	260
QY	980	ACTCAGCTAGATAGCTCAGATATGCAAGATGTCTTTGGAGGCCACAGAACTCTGGTG	1039
DB	261	ThrHisAlaArgIleGlyGlnIleCysLysAsnAspPheGlyGlyHisArgSerLeuVal	280

QY	1040	AATAAATGGACACACATTCCTCAAGCTCGTGTGATTTGCTCAGTGCCAGGTCCTCAATGGC	1099
DB	281	AsnLysTrpThrThrPheLeuLysAlaArgLeuIleCysSerValProGlyProAsnGly	300
QY	1100	ATTGACACTCATTTTGATGAAGTGCAGGATGTATTCTTAATGAACCTTTAAAGATCCTAAA	1159
DB	301	IleAspThrHisPheAspGluLeuGlnAspValPheLeuMetAsnPheLysAspProLys	320
QY	1160	AATCCAGTTGTATATGAGTGTGTTTACGACTTCCAGTAAACATTTTCAAGGGATCAGCCGTG	1219
DB	321	AsnProValValTyrGlyValPheThrThrSerSerAsnIlePheLysGlySerAlaVal	340
QY	1220	TGTATGTATAGCATGAGTGTGAGAGGGTGTCTTGGTCCATATGCCACAGGAT	1279
DB	341	CysMetTyrSerMetSerAspValArgValPheLeuGlyProTyrAlaHisArgAsp	360
QY	1280	GGACCCAACTATCAATGGTGCCTTATCAAGGAAGAGTCCCTATCCACGGCCCAAGAACT	1339
DB	361	GlyProAsnTyrGlnTrpValProTyrGlnGlyArgValProTyrProArgProGlyThr	380
QY	1340	TGTCCAGCAAAACATTTGGTGGTTTTCACCTCTACAAAGGACCTTCTCTGATGATTTATA	1399
DB	381	CysProSerLysThrPheGlyPheAspSerThrLysAspLeuProAspAspValIle	400
QY	1400	ACCTTTTGCAGGAAGTCACTCCAGCCATGTACAATCCAGTGTCTTCTATGAACAATCGCCA	1459
DB	401	ThrPheAlaArgSerHisProAlaMetTyrAsnProValPheProMetAsnAsnArgPro	420
QY	1460	ATAGTATCAAAACGGATGTAAATTTATCAATTTACAAAATGTCGTAGACCGAGTGGAT	1519
DB	421	IleValIleLysThrAspValAsnTyrGlnPheThrGlnIleValValAspArgValAsp	440
QY	1520	GCAGAAAGTGGACAGTGTATGTTATTCGGAACAGATGTGGGACCGCTTCTTAAA	1579
DB	441	AlaGluAspGlyGlnTyrAspValMetPheIleGlyThrAspValGlyThrValLeuLys	460
QY	1580	GTAGTTTCAATTCCTAAGGAGACTTGGTATGATTTAGNAGAGGTTCTGCTGGAAGAAATG	1639
DB	461	ValValSerIleProLysGluThrTrpTyrAspLeuGluValLeuLeuGluGluMet	480
QY	1640	ACAGTTTTCGGGAAACCGACTGTATTTTACAGCAATGGAAGTTCCTCACTAAGACAGCAACA	1699
DB	481	ThrValPheArgGluProThrAlaIleSerAlaMetGluLeuSerThrLysGlnGln	500
QY	1700	CTATATTTGTTTCAACCGCTGGGTTCCCGAGCTCCCTTTTACACCGGTGTGATTTTAC	1759
DB	501	LeuTyrIleGlySerThrAlaGlyValAlaGlnLeuProLeuHisArgCysAspIleTyr	520
QY	1760	GGGAAAGCGCTGTGCTGAGTGTGCTCGCCGAGACCTTACTGTGCTTGGGATGGTTCT	1819
DB	521	GlyLysAlaCysAlaGluCysLeuAlaArgAspProTyrCysAlaIleTrpAspGlySer	540
QY	1820	GCATGTTCTCGTATTTTCCACCTGCAAGAGAGAGCGCAAGACGACAAAGATATAGAAAT	1879
DB	541	AlaCysSerArgTyrPheProThrAlaLysArgArgThrArgArgGlnAspIleArgAsn	560
QY	1880	GGAGACCCACTGACCTGCTTACAGCTTACACCATGATATACCATGCGCCACAGCCCT	1939
DB	561	GlyAspProLeuThrHisCysSerAspLeuHisHisAspAsnHisHisGlyHisSerPro	580
QY	1940	GAAAGAGATCATCTATGTTGTGTAGAGATAGTAGCAGCATTTTGGAAATGCAGTCCGAAG	1999
DB	581	GluGluArgIleIleTyrGlyValGluAsnSerSerThrPheLeuGluCysSerProLys	600
QY	2000	TCCGACAGAGCGCTGCTTATTTGGCAATTCAGAGGGGAAATGAAAGAGCAAGAGAG	2059
DB	601	SerGlnArgAlaLeuValTyrTrpGlnPheGlnArgArgAsnGluArgLysGluGlu	620
QY	2060	ATCAGAGTGGATGATCATCATCAGACAGATCAAGCCCTTCTGCTACCTAGCTTACAA	2119
DB	621	IleArgValAspAspHisIleIleArgThrAspGlnGlyLeuLeuLeuArgSerLeuGln	640

```
QY 2120 CAGAAGATTACGGCAATTAACCTCTGCCATGCGGTGGAGACATGGGTTCATACAAACTCTT 2179
Db 641 GlnLysAspSerGlyAsnTyrLeuCysHisAlaValGluHisGlyPheIleGlnThrLeu 660
QY 2180 CTTAAGGTAACCTGGAAGTCATTGACACAGAGCATTTCGAGAAGCTTTTCATTAAGAT 2239
Db 661 LeuLysValThrLeuGluValIleAspThrGluHisLeuGluGluLeuLeuHisLysAsp 680
QY 2240 GATGATGGAGATGGCTCTTAAGACCAAGAAATGTCCTCAATAGCATGACACTAGCCAGAAG 2299
Db 681 AspAspGlyAspGlySerLysThrLysGluMetSerAsnSerMetThrProSerGlnLys 700
QY 2300 GTCTGTACAGAGACTTCATGAGCTCATCAACACCCCACTCAACACGATGATGAG 2359
Db 701 ValTrpTyrArgAspPheMetGlnLeuIleAsnHisProAsnLeuAsnThrMetAspGlu 720
QY 2360 TTCTGTGAACAAGCTTTGGAAAGGGACCGCAAAACCAACGTCGGCAAGGCCAGCATACC 2419
Db 721 PheCysGluGlnValTrpLysArgAspArgLysGlnArgArgGlnArgProGlyHisThr 740
QY 2420 CCAGGGAACAGTAACAAATGGAAGCACTTACAGAAATATAGAAAGGTAGAAACAGGAG 2479
Db 741 ProGlyAsnSerAsnLysTrpLysHisLeuGlnGluAsnLysLysGlyArgAsnArgArg 760
QY 2480 ACCACGAATTTGAGAGGGCACCCAGGAGTGTC 2512
Db 761 ThrHisGluPheGluArgAlaProArgSerVal 771

RESULT 2
US-08-835-268-54
; Sequence 54, Application US/08835268
; Patent No. 5807826
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey S.
; APPLICANT: Kolodkin, Alex L.
; APPLICANT: Matthes, David
; APPLICANT: Bentley, David R.
; APPLICANT: O'Connor, Timothy
; TITLE OF INVENTION: The Semaphorin Gene Family
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 Bush Street, Suite 3200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/835,268
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/121,713
; FILING DATE: 13-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B94-002-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)343-4341
; TELEFAX: (415) 343-4342
; TELEX:
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 771 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
```

```
US-08-835-268-54
Alignment Scores:
Pred. No.: 0 Length: 771
Score: 4201.00 Matches: 771
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 85.80% Indels: 0
DB: 1 Gaps: 0

US-09-774-490-1 (1-2709) x US-08-835-268-54 (1-771)
QY 200 ATGGGCTGGTTAACTAGGATTGCTGCTTTCTGGGAGATATTACTTACAGCAAGACGA 259
Db 1 MetGlyTrpLeuThrArgIleValCysLeuPheTrpGlyValLeuLeuThrAlaArgAla 20
QY 260 AACTATCAGATGGGAAGAACAAATGTGCCAAGGCTGAATATCCTCAAGAAGAAATGTTG 319
Db 21 AsnTyrGlnAsnGlyLysAsnAsnValProArgLeuLysLeuSerTyrLysGluMetLeu 40
QY 320 GAATCCAAACAATGTGATCAGCTTTCAATGGCTTGGCCCAACAGCTCCAGTTATCATACCTTC 379
Db 41 GluSerAsnAsnValIleThrPheAsnGlyLeuAlaAsnSerSerTyrHisThrPhe 60
QY 380 CTTTGTGATGAGGAACGGAGTAGGCTGTATGTGGAGCAAGGATCATCATATTTTCATTC 439
Db 61 LeuLeuAspGluGluArgSerArgLeuTyrValGlyAlaLysAspHisIlePheSerPhe 80
QY 440 GACCTGCTTAATATCAAGGATTTTCAAAAGATTGTGTGGCCAGTATCTTACACCAGAAGA 499
Db 81 AspLeuValAsnIleLysAspPheGlnLysIleValTrpProValSerTyrThrArgArg 100
QY 500 GATGAATGCAAGTGGGCTGGAAGAAGACATCTCTGAAGAATGTCTAATTTTCATCAAGTA 559
Db 101 AspGluCysLysTrpAlaGlyLysAspIleLeuLysGluCysAlaAsnPheIleLysVal 120
QY 560 CTTAAGGCATATATCAGACTCAGCTTGTACGCTGTGGAACGGGGCTTTTTCATCCAATT 619
Db 121 LeuLysAlaTyrAsnGlnThrHisLeuTyrAlaCysGlyThrGlyAlaPheHisProIle 140
QY 620 TGCACCTACATTTGAATTTGACATCATCTCGAGACAAATATTTTAAGCTGGAGAACTCA 679
Db 141 CysThrTyrIleGluIleGlyHisHisProGluAspAsnIlePheLysLeuGluAsnSer 160
QY 680 CATTTTCAAAACGGCGTGGGAAGTCCATATGACCTTAAGCTTGCTGACAGCATCCCTT 739
Db 161 HisPheGluAsnGlyArgGlyLysSerProTyrAspProLysLeuLeuThrAlaSerLeu 180
QY 740 TTAATAGATGAGAATATATACTCTGGAACCTGCAGCTGATTTTATGGGGCGAGACTTTGCT 799
Db 181 LeuIleAspGlyGluLeuTyrSerGlyThrAlaAlaAspPheMetGlyArgAspPheAla 200
QY 800 ATCTTCGGAACCTCTTGGGACACCAACCCCAATCAGACAGACAGCATGATTCAGGTGG 859
Db 201 IlePheArgThrLeuGlyHisHisProIleArgThrGluGlnHisAspSerArgTrp 220
QY 860 CTCATGATCCAAAGTTTCATTAGTGGCCACTCATCTCAGAGAGTGCACATCTCGAAGAT 919
Db 221 LeuAsnAspProLysPheIleSerAlaHisLeuIleSerGluSerAspAsnProGluAsp 240
QY 920 GACAAAGTATACCTTTTCTTCCTGAAAATGCAATAGATGGAGAACACACTCTGAAAAGCT 979
Db 241 AspLysValTyrPhePheArgGluAsnAlaIleAspGlyGluHisSerGlyLysAla 260
QY 980 ACTCACGCTAGATAGTTCAGATATCAAGAATGACTTTGGAGGGCACAGAACTCTGGTG 1039
Db 261 ThrHisAlaArgIleGlyGlnIleCysLysAsnAspPheGlyGlyHisArgSerLeuVal 280
QY 1040 AATAATGGACAACATTCCTCAAAGCTCGTCTGATTGCTAGTGGCAGGTCCAAATGGC 1099
Db 281 AsnLysTrpThrThrPheLeuLysAlaArgLeuIleCysSerValProGlyProAsnGly 300
QY 1100 ATTGACACTCATTTTGTGATGACTGCAGGATGTTATCTCTAATGAACTTAAAGATCCTAAA 1159
```

Db 301 ILeAspThrHisPheAspGluLeuGlnAspValPheLeuMetAsnPhenylsAspProlys 320
 QY 1160 AATCAGTGTATATGAGGTGTTTACAGCTTCAGTAACTTTCAGGATCAGCCGTG 1219
 Db 321 AsnProValValTyrGlyValPheThrThrSerSerAsnIlePheLysGlySerAlaVal 340
 QY 1220 TGTATGTATAGCATGAGTATGAGAGGGTCTCTTGGTCCATATCCACACAGGAT 1279
 Db 341 CysMetTyrSerMetSerAspValArgValPheLeuGlyProTyrAlaHisArgAsp 360
 QY 1280 GGACCCCAACTCAATCGGTCCTTATCAAGAGAGAGTCCCTTCCAGCGCCAGGAAT 1339
 Db 361 GlyProAsnTyrGlnTrpValProTyrGlnGlyArgValProTyrProArgProGlyThr 380
 QY 1340 TGTCGCCAGCAAAACATTTGGTGTGTTGACTCTACAAAGGAGCTTCCTGATGATGTTATA 1399
 Db 381 CysProSerLysThrPheGlyGlyPheAspSerThrLysAspLeuProAspValIle 400
 QY 1400 ACCTTTCAGAGAGATCATCCAGCATGTACATCCAGTGTTCCTTCCATGACCAATCGCCA 1459
 Db 401 ThrPheAlaArgSerHisProAlaMetTyrAsnProValPheProMetAsnAsnArgPro 420
 QY 1460 ATAGTGATCAAAACGAGATGAATATTCAATTTACAAATTTGCTAGACCGAGTGGAT 1519
 Db 421 IleValIleLysThrAspValAsnTyrGlnPheThrGlnIleValIleAspArgValAsp 440
 QY 1520 GCAGAGATCGACAGTATGATGTATGTTTATCGGAACAGATGTTGGACCGTTCCTTAAA 1579
 Db 441 AlaGluAspGlyGlnTyrAspValMetPheIleGlyThrAspValGlyThrValLeuLys 460
 QY 1580 GTAGTTCATTCCTAAGAGAGCTTGATGATGTTTGAAGAGGTCTCTCGTGAAGAATG 1639
 Db 461 ValValSerIleProLysGlnThrTrpTyrAspLeuGluGluValLeuLeuGlnMet 480
 QY 1640 ACAGTTCCTCGGAACCGACTGCTATTTCAGCAATGGAGCTTCCACTAAGCAGCAACAA 1699
 Db 481 ThrValPheArgGluProThrAlaIleSerAlaMetGluLeuSerThrLysGlnGln 500
 QY 1700 CTATATATTCGTTCAACGGCTGGGTGCCAGCTCCCTTTACACGGTGTGATATTAC 1759
 Db 501 LeuTyrIleGlySerThrAlaGlyValAlaGlnLeuProLeuHisArgCysAspIleTyr 520
 QY 1760 GGGAAACGGTCTGCTGAGTGTTCCTCGCCGAGACCTTACTGTGCTGGGATGGTCT 1819
 Db 521 GlyLysAlaCysAlaGluCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlySer 540
 QY 1820 GCATGTTCTCGCTATTTCCTCCACTGCAAGAGACGCACAGACGACAGATATAGAAT 1879
 Db 541 AlaCysSerArgTyrPheProThrAlaLysArgA-gthrA-gArgGlnAspIleArgAsn 560
 QY 1880 GGAGACCCACTGACTGCTTTCAGACTTACACCTGATATATCACCATGGCCAGCCCT 1939
 Db 561 GlyAspProLeuThrHisCysSerAspLeuHisH-sAspAsnHisHisGlyHisSerPro 580
 QY 1940 GRAGAGATCATCATGCTGTAGAGATATGACATTTTGGATGAGTCCGAG 1999
 Db 581 GluGluArgIleIleTyrGlyValGluAsnSerThrPheLeuGluCysSerProlys 600
 QY 2000 TCACAGAGACGCTGCTTCTTGGCAATTCCAGAGCGGAAATGAAGACGGAAGAAAGAG 2059
 Db 601 SerGlnArgAlaLeuValTyrTrpGlnPheGlnAsG-A-gAsnGluGluArgLysGluGlu 620
 QY 2060 ATCAGAGTGTATGATCATATCATCAGGACAGATCAGCCCTTCTGCTAGTACTACAA 2119
 Db 621 IleArgValAspAspHisIleIleArgThrAspGlnGlyLeuLeuLeuLeuArgSerLeuGln 640
 QY 2120 CAGAGGATTCAGGCAATTCCTCTGCCATGCGGTGGAACATGGGTTTCATACAAACTCTT 2179
 Db 641 GlnLysAspSerGlyAsnTyrLeuCysHisAlaValGluHisGlyPheIleGlnThrLeu 660
 QY 2180 CTTAAGTACCTGCACTGATTCATTCACAGAGCATTTGGAGAACTTCTTCATAAGAT 2239

Db 661 LeuLysValThrLeuGluValIleAspThrGluHisLeuGluGluLeuHisLysAsp 680
 QY 2240 GATGATGGAGATGGCTTAAAGCAACCAAGAAATGTCTCAATAGCATGACACCTAGCAGAAG 2299
 Db 681 AspAspGlyAspGlySerLysThrLysGluMetSerAsnSerMetThrProSerGlnLys 700
 QY 2300 GTCGTGTACAGAGACTTCATGCGACTCATCAACACCCCAATCTCAACACGATGGATGAG 2359
 Db 701 ValTrpTyrArgAspPheMetGlnLeuIleAsnHisProAsnLeuAsnThrMetAspGlu 720
 QY 2360 TTCTGTGAACAAGTTTGGAAAAGGACCCGAAACAAACATCGCGAAAGCCAGGACATACC 2419
 Db 721 PheCysGluGlnValTrpLysArgAspArgLysGlnArgGlnArgProGlyHisThr 740
 QY 2420 CCAGGGAACAGTAACAAATGGAAGCACCTTACAAGAAAATAAGAAAGTTAGAAAACAGGAGG 2479
 Db 741 ProGlyAsnSerAsnLysTrpLysHisLeuGlnGluAsnLysLysGlyArgAsnArgArg 760
 QY 2480 ACCACGAATTTGAGAGGCGACCCAGGAGTGTCT 2512
 Db 761 ThrHisGluPheGluArgAlaProArgSerVal 771
 RESULT 3
 US-09-060-692-54
 ; Sequence 54, Application US/09060692
 ; Patent No. 5935865
 ; GENERAL INFORMATION:
 ; APPLICANT: Goodman, Corey S.
 ; APPLICANT: Kolodkin, Alex L.
 ; APPLICANT: Matthes, David
 ; APPLICANT: Bentley, David R.
 ; APPLICANT: O'Connor, Timothy
 ; TITLE OF INVENTION: The Semaphorin Gene Family
 ; NUMBER OF SEQUENCES: 100
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
 ; STREET: 268 Bush Street, Suite 3200
 ; CITY: San Francisco
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94104
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/060,692
 ; FILING DATE:
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/121,713
 ; FILING DATE: 13-SEP-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Osman, Richard A.
 ; REGISTRATION NUMBER: 36,627
 ; REFERENCE/DOCKET NUMBER: B94-002-1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 343-4341
 ; TELEFAX: (415) 343-4342
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 54:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 771 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-060-692-54
 Alignment Scores:
 Pred. No.: 0 Length: 771
 Score: 4201.00 Matches: 771
 Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 85.80% Indels: 0
DB: 2 Gaps: 0

US-09-774-490-1 (1-2709) x US-09-060-692-54 (1-771)

QY 200 ATGGGCTGTTAACTAGGATGCTCTCTTCTGGGAGTATTACTTACAGCAGAGCA 259
Db 1 MetGlyTrpLeuThrArgIleValCysLeuPheTrpGlyValLeuLeuThrAlaArgAla 20
QY 260 AACTATCAGAAATCGGGAAGCAATGTGCCAAGGCTGAAATATCTCTACAAAGAAATGTG 319
Db 21 AsnTyrGlnAsnGlyLysAsnAsnValProArgLeuLysLeuSerTyrLysGluMetLeu 40
QY 320 GAATCCAAACAATGTGATCACTTTCAATGGCTTGGCCAAACAGCTCCAGTTTATCATACCTTC 379
Db 41 GluSerAsnAsnValIleThrPheAsnGlyLeuAlaAsnSerSerTyrHisThrPhe 60
QY 380 CTTTTCGATCAGGAACGAGTAGCTGTATGTGGAGCAAGGATCACATATTTTCATTC 439
Db 61 LeuLeuAspGluArgSerArgLeuTyrValGlyAlaLysAspHisIlePheSerPhe 80
QY 440 GACCTGGTTAATCAAGGATTTTCAAAAGATTGTGTGCCAGATATCTTACACCAAGAAGA 499
Db 81 AspLeuValAsnIleLysAspPheGlnLysIleValTrpProValSerTyrThrArgArg 100
QY 500 GATGAATGCAAGTGGGCTGGAAAGACATCCTGAAAGATGTCTAAATTTTCATCAGGTA 559
Db 101 AspGluCysLysTrpAlaGlyLysAspIleLeuLysGluCysAlaAsnPheIleLysVal 120
QY 560 CTTAAGGCATTAATCAGACTCACTTGTACGCTGTGGAAACGGGGCTTTTCATCCAATT 619
Db 121 LeuLysAlaTyrAsnGlnThrHisLeuTyrAlaCysGlyThrGlyAlaPheHisProIle 140
QY 620 TGCACCTAGATGAATGGACATCATCTGAGGACAAATATTTTAAAGCTGAGAACTCA 679
Db 141 CysThrTyrIleGluIleGlyHisHisProGluAspAsnIlePheLysLeuGluAsnSer 160
QY 680 CATTTTGAACCGCGCTGGAGAGTCCATATGACCTAAGCTGCTGACACATCCCT 739
Db 161 HisPheGluAsnGlyArgGlyLysSerProTyrAspProLysLeuLeuThrAlaSerLeu 180
QY 740 TTAATAGATGGAAATATATCTCTGGAATCTGAGCTGATTTTATGGGCGAGACTTCT 799
Db 181 LeuIleAspGlyGluLeuTyrSerGlyThrAlaAlaAspPheMetGlyArgAspPheAla 200
QY 800 ATCTTCGAACTTGGGACCAACCACTCAATCAGGACAGACAGCATGATTCAGGTGG 859
Db 201 IlePheArgThrLeuGlyHisHisProIleArgThrGluGlnHisAspSerArgTrp 220
QY 860 CTCATATGATCCAAAGTTTCAATAGTCCCACTCATCTCAGAGAGTGACAATCCTCAAGAT 919
Db 221 LeuAsnAspProLysPheIleSerAlaHisLeuIleSerGluSerAspAsnProGluAsp 240
QY 920 GACAAAGTATATCTTCTCGTGAATGCAATGATGAGAGACATCTCTGGAAAGCT 979
Db 241 AspLysValTyrPhePheArgGluAsnAlaIleAspGlyGluHisSerGlyLysAla 260
QY 980 ACTCAGCTAGAAATAGGTGAGATATGCAAGAATGACTTTGGAGGGCAGAGAAGTCTGGT 1039
Db 261 ThrHisAlaArgIleGlyGlnLeuCysLysAsnAspPheGlyGlyHisArgSerLeuVal 280
QY 1040 AATAATGCAACATCTCTCAAGCTCGTCTGATTTGCTCAGTCCAGGTCCTCAATATGGC 1099
Db 281 AsnLysTrpThrThrPheLeuLysAlaArgLeuIleCysSerValProGlyProAsnGly 300
QY 1100 ATGACATCATTTTCACTGAGTGGATGATTTCTCAATGATCAATTTAAAGATCCTTAA 1159
Db 301 IleAspThrHisPheAspGluLeuGlnAspValPheLeuMetAsnPheLysAspProLys 320
QY 1160 AATCCAGTTGTATATCGAGTGTTTACGATCTCCAGTAACATTTCAAGGGATCACCGGT 1219
Db 321 AsnProValValTyrGlyValPheThrThrSerSerAsnIlePheLysGlySerAlaVal 340

QY 1220 TGTATGTATAGCATGAGTGTGAGAAGGGTGTTCCTTGGTCCATATGCCACAGGAT 1279
Db 341 CysMetTyrSerMetSerAspValArgArgValPheLeuGlyProTyrAlaHisArgAsp 360
QY 1280 GGACCCAACTATCAATGGTGCCTTATCAAGGAAGTCCCTTATCCACGCCAGGAACT 1339
Db 361 GlyProAsnTyrGlnTrpValProTyrGlnGlyArgValProTyrProArgProGlyThr 380
QY 1340 TGTCCCAAGCAAAACATTTGGTGGTTCCTTCACTTACAAAGGACCTTCTCTGATGATTATA 1399
Db 381 CysProSerLysThrPheGlyGlyPheAspSerThrLysAspLeuProAspAspValIle 400
QY 1400 ACCTTTGCAAGAAGTCAATCCAGCCATGTACATCCAGTGTTCCTTCTATGAACAATCGCCCA 1459
Db 401 ThrPheAlaArgSerHisProAlaMetTyrAsnProValPheProMetAsnAsnArgPro 420
QY 1460 ATAGTGTCAAAACCGATGTAATATCAATTTACACAAATGTCGTAGACCGAGTGGAT 1519
Db 421 IleValIleLysThrAspValAsnTyrGlnPheThrGlnIleValValAspArgValAsp 440
QY 1520 GCAGAAGATGGACAGTATGATGTTATGTTATCGGAACAGATGTTGGACCGTTCCTTAAA 1579
Db 441 AlaGluAspGlyGlnTyrAspValMetPheIleGlyThrAspValGlyThrValLeuLys 460
QY 1580 GTRGTTTCAATCCCTAAGGAGACTTGTATGATTTAGAAGGTTCTCTGCGAGAAATG 1639
Db 461 ValValSerIleProLysGluThrTrpLysAspLeuGluValLeuLeuGluGluMet 480
QY 1640 ACAGTTTTTCGGGAACCGACTGCTTATTTACAGCAATGGAGCTTTCACATAAGCAGACAA 1699
Db 481 ThrValPheArgGluProThrAlaIleSerAlaMetGluLeuSerThrLysGlnGln 500
QY 1700 CTATATATTTGTTCAACGGCTGGGGTTGCCAGCTCCCTTTACACCGGTGTATTTTAC 1759
Db 501 LeuTyrIleGlySerThrAlaGlyValAlaGlnLeuProLeuHisArgCysAspIleTyr 520
QY 1760 GGGAAAGCTGTCTGAGTGTGCTCGCCGAGACCTTACTGTCTGGGATGGTCT 1819
Db 521 GlyLysAlaCysAlaGluCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlySer 540
QY 1820 GCATGTTCTCGTATTTTCCACCTGCAAGAGAGCGCAAGAGCAAGATATAAGAAAT 1879
Db 541 AlaCysSerArgTyrPheProThrAlaLysArgArgThrArgArgGlnAspIleArgAsn 560
QY 1880 GGAGACCCACTGACTCACTGTTCAGACTTACACCATGATAATCACCATGCCACAGCCCT 1939
Db 561 GlyAspProLeuThrHisCysSerAspLeuHisHisAspAsnHisHisGlyHisSerPro 580
QY 1940 GAAGAGAGAATCATCTATGTTGATAGAGATAGTAGCACATTTTGGAAATCGAGTCCGAAG 1999
Db 581 GluGluArgIleIleTyrGlyValGluAsnSerSerThrPheLeuGluCysSerProLys 600
QY 2000 TCGCAGAGAGCGCTGGTCTATTGGCAATTCAGAGCGGAATGAGAGCGGAAGAAGAG 2059
Db 601 SerGlnArgAlaLeuValTyrTrpGlnPheGlnArgArgAsnGluGluArgLysGluGlu 620
QY 2060 ATCAGAGTGAATGATCATATCATCAGACAGATCAAGCGCTTCTGCTACCTAGTCTACAA 2119
Db 621 IleArgValAspAspHisIleIleArgThrAspGlnGlyLeuLeuLeuArgSerLeuGln 640
QY 2120 CAGAAGGATTCAGGCAATTAACCTCTGCTCGCTGGAGTGGAAATGCGGTTTCATAAACTCT 2179
Db 641 GlnLysAspSerGlyAsnTyrLeuCysHisAlaValGluHisGlyPheIleGlnThrLeu 660
QY 2180 CTTAAGGTAAACCTGGGAAGTCATTGACACAGAGCATTTGGAAGAATCTTCTCATAAAGAT 2239
Db 661 LeuLysValThrLeuGluValIleAspThrGluHisLeuGluGluLeuLeuHisLysAsp 680
QY 2240 GATGATGAGATGCTCTTAAAGCAAAAGAAATGTCCAATAGCATGACACCTGACCAAG 2299
Db 681 AspAspGlyAspGlySerLysThrLysGluMetSerAsnSerMetThrProSerGlnLys 700

QY 2300 GTCTGGTACAGAGCTTCATCAGCTCATCAACACCCCAATCTCAACAGATGGATGAG 2359
 Db 701 ValThrPyrArgGspPheMetGlnLeuIleAsnHisProAsnLeuAsnThrMetAspGlu 720
 QY 2360 TTCTGTGAACAAGTTTGGAAAAGGACCGGAAAAACAACGTGGCGGCAAGCCAGGACATACC 2419
 Db 721 PheCysGluGlnValTrrPLeArgAspArgGlnArgGlnArgGlnArgGlnArgGlnArg 740
 QY 2420 CCAGGACAGTAAACAATGAGACGCTTCAAGAAATAGAAAGGTAGAAACAGGAGG 2479
 Db 741 ProGlyAsnSerAsnLysTrpLysHisLeuGlnGlnLysGlnLysGlnLysGlnLysGln 760
 QY 2480 ACCACGAAATTTGAGAGGCGCCACCCAGGAGTGTCT 2512
 Db 761 ThrH.S.GluPheGluArgAlaProArgSerVal 771

RESULT 4
 US-08-833-391-54
 ; Sequence 54, Application US/08833391
 ; Patent No. 6013781
 ; GENERAL INFORMATION:
 ; APPLICANT: Goodman, Corey S.
 ; APPLICANT: Kolodkin, Alex L.
 ; APPLICANT: Matthes, David
 ; APPLICANT: Bentley, David R.
 ; APPLICANT: O'Connor, Timothy
 ; TITLE OF INVENTION: The Semaphorin Gene Family
 ; NUMBER OF SEQUENCES: 100
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSES: SCIENCE & TECHNOLOGY LAW GROUP
 ; STREET: 268 Bush Street, Suite 3200
 ; CITY: San Francisco
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94104

COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/833,391
 ; FILING DATE:
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/121,713
 ; FILING DATE: 13-SEP-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Osman, Richard A.
 ; REGISTRATION NUMBER: 36,627
 ; REFERENCE/DOCKET NUMBER: B94-002-1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415)343-4341
 ; TELEFAX: (415) 343-4342
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 54:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 771 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-833-391-54

Alignment Scores:
 Pred. No.: 0
 Score: 4201.00
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 85.80%
 DB: 3
 Length: 771
 Matches: 771
 Conservative: 0
 Mismatches: 0
 Indels: 0
 Gaps: 0

US-09-774-490-1 (1-2709) x US-08-833-391-54 (1-771)

QY 200 ATGGCTGGTAACTAGGATTGTTCTGTCTTTCTGGGAGTATTACTTACAGCAGACCA 259
 Db 1 MetGlyTrrPLeuThrArgIleValCysLeuPheTrpGlyValLeuLeuThrAlaArgala 20
 QY 260 AACTATCAAGATGGGAAAGCAAAATGTGCAAGGCTGAAATATTCTACAAAGAAATGTTG 319
 Db 21 AsnTyrGlnAsnGlyLysAsnAsnValProArgLeuLysLeuSerTyrLysGluMetLeu 40
 QY 320 GAATCAACAATGTGATCACTTTCAATGGCTGGCCAAACAGCTCCAGTTATCATCTTC 379
 Db 41 GluSerAsnAsnValIleThrPheAsnGlyLeuAlaAsnSerSerSerTyrHisThrPhe 60
 QY 380 CTTTGGATGAGGAGGAGTAGGCTGTGTGTGGCAAGGATGATCATATTTTCATTC 439
 Db 61 LeuLeuAspGluGluArgSerArgLeuTyrValGlyAlaLysAspHisIlePheSerPhe 80
 QY 440 GACCTGGTTATATCAAGGATTTTCAAAAGATTGTGTGGCCAGTATCTTACACCAAGA 499
 Db 81 AspLeuValAsnIleLysAspPheGlnLysIleValTrrProValSerTyrThrArgarg 100
 QY 500 GATGAATGCAAGTGGCTGGGAAAGACATCTTGAAGATGTCTAAATTCATCAAGGTA 559
 Db 101 AspGluCysLysTrrPAlaGlyLysAspIleLeuLysGluCysAlaAsnPheIleLysVal 120
 QY 560 CTTAGGCATATAATCAGACTCACTTGTACGCTGTGGAACGGGGCTTTTCATCCAAT 619
 Db 121 LeuLysAlaTrrAsnGlnThrHisLeuTyrAlaCysGlyThrGlyAlaPheHisProile 140
 QY 620 TGCACCTACATTAATGAGACATCATCTCTGAGGACATATTTTAAAGCTGAGAACTCA 679
 Db 141 CysThrTyrIleGluIleGlyHisHisProGluAspAsnIlePheLysLeuGluAsnSer 160
 QY 680 CATTTTGAAGCGGCGCTGGGAGAGTCCATATGACCTCAAGCTGTGACACATCTCCCT 739
 Db 161 HisPheGluAsnGlyArgGlyLysSerProLysAspProLysLeuLeuThrAlaSerLeu 180
 QY 740 TTAATAGATGGAGAAATTAATCTCTGGAAGTCTGAGCTGATTTTATGGGGGAGACTTGT 799
 Db 181 LeuIleAspGlyGluLeuTyrSerGlyThrAlaAlaAspPheMetGlyArgAspPheAla 200
 QY 800 ATCTTCGGAACCTTGGGACACACACCAACAGGACAGCAGCAGCATGATCCAGGTGG 859
 Db 201 IlePheArgThrLeuGlyHisHisHisProIleArgThrGluGluHisAspSerArgTrp 220
 QY 860 CTCAATGATCCAAAGTTTCAATAGTCCACCTCATCTCAGAGAGTGACAAATCCTGAAGAT 919
 Db 221 LeuAsnAspProLysPheIleSerAlaHisLeuIleSerGluSerAspAsnProGluAsp 240
 QY 920 GACAAAGTATACCTTTTCTCCGTGAAATGCAATAGATGGAGACACCTCTCGAAAAGCT 979
 Db 241 AspLysValTrrPhePheArgGluAsnAlaIleAspGlyGlyHisSerGlyLysAla 260
 QY 980 ACTCAGCTAGATAGTACGATATCAAGATGACTTTGGAGGGGACAGAAAGTCTGGTG 1039
 Db 261 ThrHisAlaArgIleGlyGlnIleCysLysAsnAspPheGlyGlyHisArgSerLeuVal 280
 QY 1040 AATAAATGGACAACATCTCCTCAAGCTCGTCTGATTTGCTCAGTCCAGCTCCAAATGCG 1099
 Db 281 AsnLysTrpThrThrPheLeuLysAlaArgLeuIleCysSerValProGlyProAsnGly 300
 QY 1100 ATTGACACTCATTTTGTATGATCACTGAGGATGTATCTCAATGAACCTTTTAAAGATCTCAA 1159
 Db 301 IleAspThrHisPheAspGluLeuGlnAspValPheLeuMetAsnPheLysAspProLys 320
 QY 1160 AATCCAGTTGTATATGAGTGTATTACACTTCCAGTAACTATTTTCAAGGATCAGCCGTG 1219
 Db 321 AsnProValValTrrGlyValPheThrThrSerSerAsnIlePheLysGlySerAlaVal 340
 QY 1220 TGTATGTATAGCATGATGATGTGACAGAGGTCTCTCTGGTCCATATGCCCCACAGGAT 1279
 Db 341 CysMetTyrSerMetSerAspValArgValPheLeuGlyProTrrAlaHisArgAsp 360
 QY 1280 GGACCCCAACTATCAATGGGTGGCTTTTCAAGGAAGAGTCCCTTATCCACGCCCGCAACT 1339

Db 361 GlyProAsnTyrGlnTrpValProTyrGlnGlyArgValProTyrProArgProGlyThr 380
QY 1340 TGCCGACGAAACATTTGGTGGTTTGTACTCTACAAAGACCTTCCTGATGATGTATA 1399
Db 381 CysProSerTyrThrPheGlyGlyPheAspSerThrLysAspLeuProAspValIle 400
QY 1400 ACCTTTGCCAAGAGTCATCCAGCCATGTACAATCCAGTGTTCCTATGAACAAATCGCCA 1459
Db 401 ThrPheAlaArgSerHisProAlaMetTyrAsnProValPheProMetAsnAsnArgPro 420
QY 1460 ATAGTGATCAAAACGAGTGTAAATATCAATTTACAAAATTTGCTAGACCGAGTGGAT 1519
Db 421 IleValIleLysThrAspValAsnTyrGlnPheThrGlnIleValValAspArgValAsp 440
QY 1520 GCAGAGATGCGACAGATGATGTATGTTTTCGGACACAGATCTTGGACCGCTTTCTAAA 1579
Db 441 AlaGluAspGlyGlnTyrAspValMetPheIleGlyThrAspValGlyThrValLeuLys 460
QY 1580 GTAGTTTCAATTCCTAAGGAGACTTGGTATGATTTAGAAAGAGTCTGCTGGAAGAAATG 1639
Db 461 ValValSerIleProLysGluThrTrpTyrAspLeuGluValLeuLeuGluMet 480
QY 1640 ACAGTTTTCGGGAACCGACTGCTATTTCCAGCAATGGAGCTTCCACTAAGCAGCAACA 1699
Db 481 ThrValPheArgGluProThrAlaIleSerAlaMetGluLeuSerThrLysGlnGln 500
QY 1700 CTATATATGGTTCAACGGCTGGGTTGCCAGCTCCCTTTACACGGTGTGATATTAC 1759
Db 501 LeuTyrIleGlySerThrAlaGlyValAlaGlnLeuProLeuHisArgCysAspIleTyr 520
QY 1760 GGAAGAGCTGTGCTGAGTGTGCTCGCCGACGACCTTACTGTCTGGGATGTTCT 1819
Db 521 GlyLysAlaCysAlaGluCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlySer 540
QY 1820 GCATGTTCTCGCTATTTCCCTGCAAGAGACGACACAGACGACACAGATATAAGAAT 1879
Db 541 AlaCysSerArgTyrPheProThrAlaLysArgThrArgGlnAspIleArgAsn 560
QY 1880 GGAGACCCACTGACTACTGTTTCAGACTTACACCATGATAATCACCATGGCCACAGCCCT 1939
Db 561 GlyAspProLeuThrHisCysSerAspLeuHisAspAsnHisGlyHisSerPro 580
QY 1940 GAAGAGAGATCATCTATGCTGTAGAGATAGTAGACACATTTTGGATGCGATCCGAG 1999
Db 581 GluGluArgIleIleTyrGlyValGluAsnSerSerThrPheLeuGluCysSerProLys 600
QY 2000 TCCGACAGACCGCTGCTCTATTGGCAATTCAGAGCGAAATGAAGAGCGAAAGACAG 2059
Db 601 SerGlnArgAlaLeuValTyrTrpGlnPheGlnArgAsnGluGluArgLysGluGlu 620
QY 2060 ATCAGATGGATGATCATATCATCAGGACAGATCAAGGCTTCTGCTACGTAGTCTCAA 2119
Db 621 IleArgValAspAspHisIleIleArgThrAspGlnGlyLeuLeuLeuArgSerLeuGln 640
QY 2120 CAGAGAGTTCAGGCAATTTACCTGCTGCAATGGTGGACATGGTTCATACAACTCTT 2179
Db 641 GlnLysAspSerGlyAsnTyrLeuCysHisAlaValGluHisGlyPheIleGlnThrLeu 660
QY 2180 CTTAAGGTAAACCTCGAAGTCTATTGACACAGACGACATTTGGAAGAACTTCTCATAAAG 2239
Db 661 LeuLysValThrLeuGluValIleAspThrGluHisLeuGluGluLeuHisLysAsp 680
QY 2240 GATGATGGAGATGCTCTAAGACCAAGAAATGTCATAGCATGACACCTAGCCAGAG 2299
Db 681 AspAspGlyAspGlySerLysThrLysGluMetSerAsnSerMetThrProSerGlnLys 700
QY 2300 GTCTGGTACAGAGACTTCATGAGCTTCATCAACACCCCAATCTCAACACCATGATGAG 2359
Db 701 ValTyrTrpArgAspPheMetGlnLeuIleAsnHisProAsnLeuAsnThrMetAspGlu 720
QY 2360 TTCTGTGAACAAGTTTGGAAAGGACCGGAAACAACTGCGCAAGCGCCAGGACATACC 2419

Db 721 PheCysGluGlnValTrpLysArgAspArgLysGlnArgGlnArgProGlyHisThr 740
QY 2420 CCAGGGAACAGTAAACAATGAAGACACTTACAGAAAAATAAGAAAGTAGAAACAGGAGG 2479
Db 741 ProGlyAsnSerAsnLysTrpLysHisLeuGlnGluAsnLysLysGlyArgAsnArgArg 760
QY 2480 ACCACCAATTTGAGAGCGCACCCAGGAGTGTCT 2512
Db 761 ThrHisGluPheGluArgAlaProArgSerVal 771
RESULT 5
US-09-060-610-54
; Sequence 54, Application US/09060610
; Patent No. 6344544
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey S.
; APPLICANT: Kolodkin, Alex L.
; APPLICANT: Matthews, David
; APPLICANT: Bentley, David R.
; APPLICANT: O'Connor, Timothy
; TITLE OF INVENTION: The Semaphorin Gene Family
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 Bush Street, Suite 3200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/060,610
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/835,268
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B94-002-1
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; TELEX:
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 771 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-060-610-54
Alignment Scores:
Pred. No.: 0 Length: 771
Score: 4201.00 Matches: 771
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 85.80% Indels: 0
DB: 4 Gaps: 0
US-09-774-490-1 (1-2709) x US-09-060-610-54 (1-771)
QY 200 ATGGGCTGGTTAACTAGGATGTCTGTTTCTGGGAGTATTACTTACAGCAAGACA 2559
Db 1 MetGlyTrpLeuThrArgIleValCysLeuPheTrpGlyValLeuLeuThrAlaArgAla 20
QY 260 AACTATCAGAAATCGGAGAACAAATGTCCAGGCTGAAATTCCTACAGAAATGTTG 319

Db 21 AsnTyrGlnAsnGlyLysAsnAsnValProArgLeuLysLeuSerTyrLysGluMetLeu 40
QY 320 GAATCCAAACATGATGATCACTTTCAATGGCTGGCCCAACAGCTCCAGTTATCATACCTTC 379
Db 41 GluSerAsnAsnValIleThrPheAsnGlyLeuAlaAsnSerSerTyrHisThrPhe 60
QY 380 CTTTGGATGAGGAACGAGTAGCTGTATGTTGGAGCAAGAGATCAATATTTTCATTC 439
Db 61 LeuLeuAspGluGluArgSerArgLeuTyrValGlyAlaLysAspHisIlePheSerPhe 80
QY 440 GACCTGTTAATATCAAGGATTTTCAAGATTTGTGGCCAGTATCTTACACCAAGA 499
Db 81 AspLeuValAsnIleLysAspPheGlnLysIleValIleThrProValSerTyrThrArg 100
QY 500 GATGAATGCAAGTGGCTGGAAAGACATCTCGAAGAAGATGTGCTAAATTTCAATCAAGGTA 559
Db 101 AspGluCysIleThrAlaGlyLysAspIleLeuLysGluCysAlaAsnPheIleLysVal 120
QY 560 CTTAAGGCATATATCAAGACTCACTGTAGCTGTGGAAACGGGGCTTTTCATCCAATT 619
Db 121 LeuLysAlaTyrAsnGlnThrHisLeuTyrAlaCysGlyThrGlyAlaPheHisProIle 140
QY 620 TGCACTTACATGAATTTGACATCATCTCGAGGACAAATATTTTAACTGGAGAACTCA 679
Db 141 CysThrTyrIleGluIleGlyHisHisProGluAspAsnIlePheLysLeuGluAsnSer 160
QY 680 CATTTTCARACCGCTGGAGAGTCCATATGACCTTAAGCTCTGACAGCATCCCTT 739
Db 161 HisPheGluAsnGlyArgGlyLysSerProTyrAspProLysLeuThrAlaSerLeu 180
QY 740 TTAATAGATGGAATATATCTCGAAGTGCAGCTGATTTTATGGGCGAGACTTCTCT 799
Db 181 LeuIleAspGlyGluLeuTyrSerGlyThrAlaAlaAspPheMetGlyArgAspPheAla 200
QY 800 ATCTCCGAAGCTCTGGGACACCAACCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 859
Db 201 IlePheArgThrLeuGlyHisHisHisProIleArgThrGluGluHisAspSerArgIle 220
QY 860 CTCATGATCCAAAGTTCATTAAGTCCCACTCATCTCAGAGATGCAATCTCGAAGAT 919
Db 221 LeuAsnAspProLysPheIleSerAlaHisLeuIleSerGluSerAspAsnProGluAsp 240
QY 920 GACAAATGATCTTTCTTCCTGGAATGCAATGAGATGAGAGACATCTCGAAGACT 979
Db 241 AspLysValIlePhePheArgGluAsnAlaIleAspGlyGluHisSerGlyLysAla 260
QY 980 ACTCACGCTAGATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1039
Db 261 ThrHisAlaArgIleGlyGlnIleCysLysAsnAspPheGlyHisArgSerLeuVal 280
QY 1040 AATAAATGGAACAATCTCCAAAGCTCTGATTTGCTCAGTCCAGGTCCTCAATGGC 1099
Db 281 AsnLysTrpThrPheLeuLysAlaArgLeuIleCysSerValProGlyProAsnGly 300
QY 1100 ATTGACACTCATTTGATGAAGTGCAGGATGATTTCTTAATGAATTTAAAGATCTTAA 1159
Db 301 IleAspThrHisPheAspGluLeuGlnAspValPheLeuMetAsnPheLysAspProLys 320
QY 1160 AATCCAGTGTATAGAGTGTATAGACTTCCAGTCCAGTATCAATTTCAAGGATCAGCGTG 1219
Db 321 AsnProValValIleGlyValPheThrThrSerSerAsnIlePheLysGlySerAlaVal 340
QY 1220 TGTATGATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1279
Db 341 CysMetTyrSerMetSerAspValArgValPheLeuGlyProTyrAlaHisArgAsp 360
QY 1280 GGAACCAACTCATCAATGGTGCCTTATCAAGAGAGTCCCTATCCAGGCGCAGGACT 1339
Db 361 GlyProAsnTyrGlnIleThrValProTyrGlnGlyArgValProTyrProArgProGlyThr 380
QY 1340 TGTCACGACAAAACATTTGGTGGTTTGTACTTACAAAGGACCTTCTCATGATGATGATA 1399
Db 381 CysProSerLysThrPheGlyGlyPheAspSerThrLysAspLeuProAspValIle 400

QY 1400 ACCTTTGCAAGAGTCAATCCAGCATGTACATCCAGTGTTCCTATGAACAATCGCCCA 1459
Db 401 ThrPheAlaArgSerHisProAlaMetTyrAsnProValPheProMetAsnAsnArgPro 420
QY 1460 ATAGTATCAAAACCGATGTAAATTTATCAATTTACAAATTTGCTGAGACCGAGTGGAT 1519
Db 421 IleValIleLysThrAspValAsnTyrGlnPheThrGlnIleValValAspArgValAsp 440
QY 1520 GCAGAAGATGCAACAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1579
Db 441 AlaGluAspGlyGlnTyrAspValMetPheIleGlyThrAspValGlyThrValLeuLys 460
QY 1580 GTAGTTTCATTTCCCTAAGGAGACTTGGTATGATTTAGAGAGGTTCTGCTGGAAGAATG 1639
Db 461 ValValSerIleProLysGluThrTrpTyrAspLeuGluValLeuLeuGluMet 480
QY 1640 ACAGTTTTCGGGAACCGACTGCTATTTTCAGCAATGAGCTTTCCACTAAGCAGCAACA 1699
Db 481 ThrValPheArgGluProThrAlaIleSerAlaMetGluLeuSerThrLysGlnGln 500
QY 1700 CTATATTTGTTTCAACGGCTGGGTTCCTCCAGCTCCCTTTACACCGGTGTATTTAC 1759
Db 501 LeuTyrIleGlySerThrAlaGlyValAlaGlnLeuProLeuHisArgCysAspIleTyr 520
QY 1760 GGGAAAGCGTGTCTGAGTGTCTGCTCCCGAGACCTTACTGTCTTGGGATGGTTCT 1819
Db 521 GlyLysAlaCysAlaGluCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlySer 540
QY 1820 GCATGTTCTCGCTATTTTCCCACTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1879
Db 541 AlaCysSerArgTyrPheProThrAlaLysArgArgThrArgGlnAspIleArgAsn 560
QY 1880 GGAGACCCACTGACTCACTGTTTCAGACTTACACCATGATATACCATGATGATGATGATG 1939
Db 561 GlyAspProLeuThrHisCysSerAspLeuHisHisAspAsnHisHisGlyHisSerPro 580
QY 1940 GAAGAGAGATCATCTTATGTTGATGATGATGATGATGATGATGATGATGATGATGATG 1999
Db 581 GluGluArgIleIleTyrGlyValGluAsnSerSerThrPheLeuGluCysSerProLys 600
QY 2000 TCGAGAGAGCGCTGCTCTATTGGCAATTCAGAGGCGAATGAAGAGAGAGAGAGAGAG 2059
Db 601 SerGlnArgAlaLeuValTyrTrpGlnPheGlnArgAsnGluGluArgLysGluGlu 620
QY 2060 ATCAGAGTGGATGATCATCATCAGGACAGATCAAGCCCTTCTGCTACGTAGCTACAA 2119
Db 621 IleArgValAspAspHisIleArgThrAspGlnGlyLeuLeuLeuArgSerLeuGln 640
QY 2120 CAGAGAGTTCAGGCAATTTACTCTGCTCCATCGGTGGAACATGGTTTCATCAAACTCTT 2179
Db 641 GlnLysAspSerGlyAsnTyrLeuCysHisAlaValGluHisGlyPheIleGlnThrLeu 660
QY 2180 CTTAAGGTAACCTCGAAGTCAATTCACAGAGATTTGGAAGACTTCTTCATTAAGAT 2239
Db 661 LeuLysValThrLeuGluValIleAspThrGluHisLeuGluGluLeuLeuHisLysAsp 680
QY 2240 GATGATGAGATGCTCTTAAGACCAAAAGATGTCCAATAGCATGACACCTAGCCAGAAG 2299
Db 681 AspAspGlyAspGlySerLysThrLysGluMetSerAsnSerMetThrProSerGlnLys 700
QY 2300 GTCTGGTACAGAGACTTCATGACGCTCATCAACCAACCCCAATCTCAACAGATGGATGAG 2359
Db 701 ValTrpTyrArgAspPheMetGlnLeuIleAsnHisProAsnLeuAsnThrMetAspGlu 720
QY 2360 TTCTGTGAACAAAGTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2419
Db 721 PheCysGluGlnValTrpLysArgAspArgLysGlnArgGlnArgProGlyHisThr 740
QY 2420 CCAGGAAACAGTAAACAAATGGAAGCATTACAGAAATTAAGAAAGTGAAGACAGGAGG 2479
Db 741 ProGlyAsnSerAsnLysTrpLysHisLeuGlnGluAsnLysLysGlyArgAsnArgArg 760

QY 2480 ACCACGAATTTGAGAGGACCCAGAGTGC 2512
 Db 761 ThrHisGluPheGluAraGalaProArgSerVal 771

RESULT 6

PCT-US94-10151A-54
 ; Sequence 54, Application PC/TUS9410151A
 ; GENERAL INFORMATION:
 ; APPLICANT: The Regents of the University of California
 ; TITLE OF INVENTION: The Semaphorin Gene Family
 ; NUMBER OF SEQUENCES: 66
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: FLEHR HOCHBACH TEST ALBRITTON & HERBERT
 ; STREET: 4 Embarcadero Center, Suite 3400
 ; CITY: San Francisco
 ; STATE: CA

; COUNTRY: USA
 ; ZIP: 94111-4187
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US94/10151A
 ; FILING DATE: 13-SEP-1994
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Osman, Richard A.
 ; REGISTRATION NUMBER: 36,627
 ; REFERENCE/DOCKET NUMBER: FP-58750-PC/RAO
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 781-1989
 ; TELEFAX: (415) 398-3249
 ; TELEX: 910 277299 FHT UR
 ; INFORMATION FOR SEQ ID NO: 54:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 771 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; PCT-US94-10151A-54

Alignment Scores:

Pred. No.: 0 Length: 771
 Score: 4201.00 Matches: 771
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 85.80% Indels: 0
 DB: 5 Gaps: 0

US-09-774-490-1 (1-2709) x PCT-US94-10151A-54 (1-771)

QY 200 ATGGGCTGTTAACTAGGATTCGTCTTTCTGGGAGTATTACTTACAGCAGACA 259
 Db 1 MetGlyTrpThrArgIleValCysLeuPheTrpGlyValLeuLeuThrAlaGala 20
 QY 260 AACTATCAGATGGGAGAACAAATGTGCCAAGCTGAAATATTCCTACAAAGAAATGTG 319
 Db 21 AsnTyrGlnAsnGlyLysAsnValProArgLeuLysLeuSerTyLysGluMetLeu 40
 QY 320 GAATCCAAATGTGATCACTTTCATGCTGGCTGGCCACAGCTCCAGTTATCATACCTTC 379
 Db 41 GluSerAsnAsnValIleThrPheAsnGlyLeuAlaAsnSerSerTyHisThrPhe 60
 QY 380 CTTTGGATGAGGAACGGAGTAGGCTGTATGTGGAGCAAGGATCACATATTTTCATTC 439
 Db 61 LeuLeuAspGluArgSerArgLeuTyrValGlyAlaLysAspHisIlePheSerPhe 80
 QY 440 GACCTGGTTAATATCAAGATTTTCAAAGATTTGTGGCCAGTATCTTACACGAAGA 499
 Db 81 AspLeuValAsnIleLysAspPheGlnLysIleValTrpProValSerTyThrArg 100

QY 500 GATGAATGCAAGTGGCTGGAAAAAGACATCTCTGAAAGAAATGTCTAATTTCAATCAAGTA 559
 Db 101 AspGluCysLysTrpAlaGlyLysAspIleLeuLysGluCysAlaAsnPheIleLysVal 120
 QY 560 CTTAAGGCATATAATCAGACTCACTGTAGCCCTGTGGAACGGGGCTTTTTCATCCAATT 619
 Db 121 LeuLysAlaTyrAsnGlnThrHisLeuTyrAlaCysGlyThrGlyAlaPheHisProIle 140
 QY 620 TGCACCTACATTTGAAATTTGGACATCATCTGAGGACAAATATTTTAAAGCTGGAGAACTCA 679
 Db 141 CysThrTyrIleGluIleGlyHisHisProGluAspAsnIlePheLysLeuGluAsnSer 160
 QY 680 CATTTTGAACACGGCGCTGGAGAGTCCATATGACCTACCTAGCTGCTGACAGCATCCCTT 739
 Db 161 HisPheGluAsnGlyArgGlyLysSerProTyrAspProLysLeuLeuThrAlaSerLeu 180
 QY 740 TTAATAGATGGAGAAATTATATCTCTGGAACCTGCAGCTGATTTTATGGGGCGAGACTTTGCT 799
 Db 181 LeuIleAspGlyGluLeuTyrSerGlyThrAlaAlaAspPheMetGlyArgAspPheAla 200
 QY 800 ATCTTCGAACTCTTGGCCACCACCCCAATCAGGACAGACAGCATGATTCAGGTGG 859
 Db 201 IlePheArgThrLeuGlyHisHisHisProIleArgThrGluGlnHisAspSerArgTrp 220
 QY 860 CTCAATGATCCAAAGTTTCATTAGTGGCCACCTCATCTCAGAGAGTGACATCTCTGAAGAT 919
 Db 221 LeuAsnAspProLysPheIleSerAlaHisLeuIleSerGluSerAspAsnProGluAsp 240
 QY 920 GACAAAGTATACTTTTCTCCGTGAAAAATGCAATAGATGGAGAACACTCTGGAAGACT 979
 Db 241 AspLysValTyrPhePhePheArgGluAsnAlaIleAspGlyGluHisSerGlyLysAla 260
 QY 980 ACTCACCTAGATAGTTCAGATATGCAAGAATGACTTTGAGGGGACAGAAAGTCTGGT 1039
 Db 261 ThrHisAlaArgIleGlyGlnIleCysLysAsnAspPheGlyGlyHisAspSerLeuVal 280
 QY 1040 AATAAATGGACAAACATTCCTCAAAGCTCGTCTGATTTGCTCAGTGCAGGTCCAAATGGC 1099
 Db 281 AsnLysTrpThrThrPheLeuLysAlaArgLeuIleCysSerValProGlyProAsnGly 300
 QY 1100 ATTGACACTCATTTTGATGAACCTGCAGGATGTATCTCTAATGAACITTAAGATCCTAAA 1159
 Db 301 IleAspThrHisPheAspGluLeuGlnAspValPheLeuMetAsnPheLysAspProLys 320
 QY 1160 AATCCAGTGTATATGAGTGTATTACGACTTCAGTAAACATTTTCAAGGATCAGCGGTG 1219
 Db 321 AsnProValValTyrGlyValPheThrThrSerSerAsnIlePheLysGlySerAlaVal 340
 QY 1220 TGTATGTATAGCATGATGATGTGAGAAGGGTGTCTTGGTCCATATGCCACAGGGAT 1279
 Db 341 CysMetTyrSerMetSerAspValArgValPheLeuGlyProTyrAlaHisArgAsp 360
 QY 1280 GGACCCCAACTATCAATGGGTGCCTTATCAAGGAAGAGTCCCTCATCCACGGCCAGGAAC 1339
 Db 361 GlyProAsnTyrGlnTrpValProTyrGlnGlyArgValProTyrProArgProGlyThr 380
 QY 1340 TGTCCTCCAGCAAAACATTTGGTGGTTTTGACTCTACAAAGGACCTTCCTGATGATGTATA 1399
 Db 381 CysProSerLysThrPheGlyGlyPheAspSerThrLysAspLeuProAspAspValIle 400
 QY 1400 ACCTTTTGCAGAAGATCATCCAGCCATGTACAAATCCAGTGTCTTCTATGAACAATCGCCA 1459
 Db 401 ThrPheAlaArgSerHisProAlaMetTyrAsnProValPheProMetAsnAsnArgPro 420
 QY 1460 ATAGTGATCAAAACGGATGTAAATTTATCAATTTACACAAATTCCTGTAGACCCAGTGGAT 1519
 Db 421 IleValIleLysThrAspValAsnTyrGlnPheThrGlnIleValValAspArgValAsp 440
 QY 1520 GCGAAGATCGACAGATGATGATGTATGTTATCGGAACAGATGTTGGACCGCTCTTAA 1579
 Db 441 AlaGluAspGlyGlnTyrAspValMetPheIleGlyThrAspValGlyThrValLeuLys 460
 QY 1580 GTAGTTTCAATTCTTAAGGAGACTTGGTATGATTTTAGAAGAGGTTCTGTGGAGAAATG 1639

```

; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING CD100 MOLECULES
; FILE REFERENCE: DFN-005CPA2
; CURRENT APPLICATION NUMBER: US/08/556,422A
; CURRENT FILING DATE: 1995-11-09
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 655
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-08-556-422A-3

Alignment Scores:
Pred. No.: 0 Length: 655
Score: 3568.00 Matches: 655
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 72.88% Indels: 0
DB: 4 Gaps: 0

US-09-774-490-1 (1-2709) x US-08-556-422A-3 (1-655)

Db 461 ValValSerLeuProLysGluThrTrpTyrAspLeuGluGluValLeuLeuGluMet 480
Qy 1640 ACAGTTTTCGGGAACCACTGCTATTTTACAGCAATGGAGCTTCCACAAAGCAGCAACAA 1699
Db 481 ThrValPheArgGluProThrAlaIleSerAlaMetGluLeuSerThrLysGlnGln 500
Qy 1700 CTATATATTGGTTCACCGCTGGGTTGCCAGCTCCCTTTTACACGGTGTGATATTAC 1759
Db 501 LeuTyrIleGlySerThrAlaGlyValAlaGlnLeuProLeuHisArgCysAspIleTyr 520
Qy 1760 GGAAGACGGTGTGCTGAGTGTTCCTCGCCGCGAGACCCCTTACTGTCTTGGGATGCTCT 1819
Db 521 GlyLysAlaCysAlaGluCysCysLeuAlaIleAspProTyrCysAlaTrpAspGlySer 540
Qy 1820 GCATGTTCTCGCTATTTTCCATCTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1879
Db 541 AlaCysSerArgTyrPheProThrAlaIleArgArgThrArgGlnAspIleArgAsn 560
Qy 1880 GGAGACCCACTGACTCACTGCTTCCAGACTTACACCATGATAATCACCATGGCCACAGCCCT 1939
Db 561 GlyAspProLeuThrHisCysSerAspLeuHisHisAspAsnHisGlyHisSerPro 580
Qy 1940 GAAGAGAGATCATCTATGTTGATAGAGATAGTAGACATTTTGGATGCGATCGGAG 1999
Db 581 GluGluArgIleIleTyrGlyValGluAsnSerSerThrPheLeuGluCysSerProLys 600
Qy 2000 TCGCAGAGAGCGCTGGTCTATTTCGCAATTCAGAGCGGAAATGAAGAGCGAAAGAGAG 2059
Db 601 SerGlnArgAlaLeuValTyrTrpGlnPheGlnArgArgAsnGluGluArgLysGluGln 620
Qy 2060 ATCAGAGTGAATCATATCATCATCAGACAGATCAAGGCTTCTGCTAGTGTCTACAA 2119
Db 621 IleArgValAspAspHisIleIleArgThrAspGlnGlyLeuLeuLeuArgSerLeuGln 640
Qy 2120 CAGAAGGATTTCAGGCAATTAACCTCTGCTGCAATGCGGTGGAACATGGGTTCATACAACTCTT 2179
Db 641 GlnLysAspSerGlyAsnTyrLeuCysHisAlaValGluHisGlyPheIleGlnThrLeu 660
Qy 2180 CTTAAGTAACTCGGAGTCAATGACACAGAGCATTTGGAAGAACTTCTTCATTAAGAT 2239
Db 661 LeuLysValThrLeuGluValIleAspThrGluHisLeuGluGluGluLeuHisLysAsp 680
Qy 2240 GATGATCGAGATGGCTCTTAAGACCAAGAAATGTCATATAGCATGACACCTAGCCAGAG 2299
Db 681 AspAspGlyAspGlySerLysThrLysGluMetSerAsnSerMetThrProSerGlnLys 700
Qy 2300 GTCTGTTACAGAGACTTCATGAGCTCATCAACCCACCCCAATCTCAACAGATGGATGAG 2359
Db 701 ValTrpTyrArgAspPheMetGlnLeuIleAsnHisProAsnLeuAsnThrMetAspGlu 720
Qy 2360 TTCTGTCAACAAGTTTGGAAAGGGACCGAAACCAAGTCGGGCAAGGCCAGGACATACC 2419
Db 721 PheCysGluGlnValTrpLysArgAspArgLysGlnArgGlnArgProGlyHisThr 740
Qy 2420 CACGGGAACAGTAACTAAGAGAGCACTTACAGAAATATAGAAAGGTAGAAACAGGAGG 2479
Db 741 ProGlyAsnSerAsnLysTrpLysHisLeuGlnGluAsnLysLysGlyArgAsnArgArg 760
Qy 2480 ACCCAGCAATTTGAGAGGGCCAGCCAGGAGTGTCT 2512
Db 761 ThrHisGluPheGluArgAlaProArgSerVal 771

```

RESULT 7

```

; Sequence 3, Application US/08556422A
; Patent No. 6576754
; GENERAL INFORMATION:
; APPLICANT: HALL, Kathryn T.
; APPLICANT: FREEMAN, Gordon J.
; APPLICANT: SCHULTZE, Joachim L.
; APPLICANT: BOUSSELOTIS, Vassiliki
; APPLICANT: NADLER, Lee M.

```

```

; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING CD100 MOLECULES
; FILE REFERENCE: DFN-005CPA2
; CURRENT APPLICATION NUMBER: US/08/556,422A
; CURRENT FILING DATE: 1995-11-09
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 655
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-08-556-422A-3

Alignment Scores:
Pred. No.: 0 Length: 655
Score: 3568.00 Matches: 655
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 72.88% Indels: 0
DB: 4 Gaps: 0

US-09-774-490-1 (1-2709) x US-08-556-422A-3 (1-655)

Qy 200 ATGGGCTGTTAACTAGGATTTGCTCTTCTTCTGGGAGTATTACTTACAGCAGAGCA 259
Db 1 MetGlyTyrLeuThrArgIleValCysLeuPheTrpGlyValLeuLeuThrAlaArgAla 20
Qy 260 AACTATCAGAATGGGAAGAACAAATGTGCCAAGGCTGAAATATTCTCAAGAAATCTTG 319
Db 21 AsnTyrGlnAsnGlyLysAsnAsnValProArgLeuLysLeuSerTyrLysGluMetLeu 40
Qy 320 GAATCCACAATGTCATCACTTCAATGCTTCAATGCTTGGCCACAGCTCCAGTATCATACCTC 379
Db 41 GluSerAsnAsnValIleThrPheAsnGlyLeuAlaAsnSerSerSerTyrHisThrPhe 60
Qy 380 CTTTGGATGAGAAACGGAGTAGGCTGTATGTTGGACCAAGGATCATATTTTTCATTC 439
Db 61 LeuLeuAspGluGluArgSerArgLeuTyrValGlyAlaLysAspHisIlePheSerPhe 80
Qy 440 GACCTGGTAAATCAAGATTTCAAGAGATTTGTTGGCCAGTATCTTACACAGAGCA 499
Db 81 AspLeuValAsnIleLysAspPheGlnLysIleValTrpProValSerTyrThrArgArg 100
Qy 500 GATGAATCAAGTGGGCTGGAAGACATCTCGAAGAAATGTCTAAATTTTCATCAAGTA 559
Db 101 AspGluCysLysTrpAlaGlyLysAspIleLeuLysGluCysAlaAsnPheIleLysVal 120
Qy 560 CTTAAGGCATATAATCAGACTCACTTGTACGCTGTGACGGGGCTTTTCATCCAAAT 619
Db 121 LeuLysAlaLysAsnGlnThrHisLeuTyrAlaCysGlyThrGlyAlaPheHisProIle 140
Qy 620 TGCACCTACATTGAAATTTGGACATCATCTCGAGGACAATATTTTAAAGCTGGAGAACTCA 679
Db 141 CysThrTyrIleGluIleGlyHisHisProGluAspAsnIlePheLysLeuGluAsnSer 160
Qy 680 CATTTTGAACCGCCCTGGGAGAGTCCATATGACCTAGCTGCTGACAGCATCCCTT 739
Db 161 HisPheGluAsnGlyArgGlyLysSerProTyrAspProLysLeuLeuThrAlaSerLeu 180
Qy 740 TTAATAGATGGAAGATTTATCTTCTGGAATCTGACGCTGATTTTATGGGCGGAGACTTGTCT 799
Db 181 LeuIleAspGlyGluLeuTyrSerGlyThrAlaAlaAspPheMetGlyArgAspPheAla 200
Qy 800 ATCTTCGAGTCTTGGGACACCCCAATCAGGACAGCAGCAGCATGATCCAGGTGG 859
Db 201 IlePheArgThrLeuGlyHisHisHisProIleArgThrGluGlnHisAspSerArgTrp 220
Qy 860 CTCAATGATCCAAAGTTTCATTAGTGGCCACCTCATCTCAGAGAGTGCATATCTCCAGAT 919
Db 221 LeuAsnAspProLysPheIleSerAlaHisLeuIleSerGluSerAspAsnProGluAsp 240
Qy 920 GACAAAGTATATCTTTCTTCTCGTGAAGATGATGAGAACACTCTGGAAGAGCT 979
Db 241 AspLysValTyrPhePhePheArgGluAsnAlaIleAspGlyGluHisSerGlyLysAla 260

```

```

QY 2060 ATCAGAGTGATGATCATATCATCAGACAGATCAGAGCCCTTCTGCTACTGCTACAA 2111
Db 621 ILAArgValAspAspHisIleIleAArgThrAspGlnGlyLeuLeuLeuAArgSerLeuGln 640
QY 2120 CAGAAGGATTACGCGCAATTACCTCTGCCATGCGGTGGAACATGGG 2164
Db 641 GlnHisAspSerGlyAsnTyrLeuCysHisAlaValGluHisGly 655

RESULT 8
US-08-136-922-2
; Sequence 2, Application US/08136922
; Patent No. 5416197
; GENERAL INFORMATION:
; APPLICANT: Raper, Jonathan A.
; APPLICANT: Luo, Yuling
; TITLE OF INVENTION: Compositions Which Regulate Neural
; TITLE OF INVENTION: Regeneration and Methods of Making and Using the Same
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESS: No. 5416197ris
; STREET: One Liberty Place
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/136,922
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: UPN-1428
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 477 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-136-922-2

Alignment Scores:
Pred. No.: 2,316-246 Length: 477
Score: 2562.00 Matches: 472
Percent Similarity: 99.37% Conservative: 0
Best Local Similarity: 99.37% Mismatches: 3
Query Match: 52.33% Indels: 0
DB: 1 Gaps: 0

US-09-774-490-1 (1-2709) x US-08-136-922-2 (1-477)
QY 899 GAGAGTGAACAATCCTGAAGATGACAAAGTATATCTTTCTTCGCGAAAAATCAATAGAT 958
Db 2 GluHisAspAsnProGluAspAspLysValTyrPhePheArgLysGluAsnAlaIleAsp 21
QY 959 GGAGAACACTCTGGAAAAGCTACTCACGCTAGAATAGTTCAGATATGCAAGAATCACTTT 1018
Db 22 GlyGluHisSerGlyLeuAlaThrHisAlaArgGlyGlnIleCysLysAsnAspPhe 41
QY 1019 GGAGGGCAGAGAAGTCTGTGTGAATAAATGGACAAACATTCCTCAAGACTCGTCTGATTGC 1078
Db 42 GlyGlyHisArgSerLeuValAsnLysTrpThrPheLeuLysAlaArgLeuIleCys 61
QY 1079 TCAGTGCAGAGGTCCAAATGGCATTGACACTCATTTTGATGAACTCAGAGATGTATCTCTA 1138

```

Db 62 SerValProGlyProAsnGlyIleAspThrHisPheAspGluLeuGlnAspValPheLeu 81
Qy 1139 ATGAACCTTTAAAGATCCATAAAATCCAGTGTATATGGAGTGTATACGACTTCCAGTAAC 1198
Db 82 MetAsnPheLysAspProLysAsnProValValValGlyValPheThrThrSerSerAsn 101
Qy 1199 ATTTTCAGGATCAGCCGCTGTATGTATAGATCAGTGTATGAGAGGCTGTCCCTT 1258
Db 102 IlePheLysGlySerAlaValCysMetTyrSerMetSerAspValArgValPheLeu 121
Qy 1259 GGTCCATATGCCACAGGGATGACCCCACTATCAATGGTGCCTTATCAAGGAAGTC 1318
Db 122 GlyProTyrAlaHisAspGlyProAsnTyrGlnTyrValProTyrGlnGlyArgVal 141
Qy 1319 CCTATCCAGCCGAGCACTTCCACGACCAACATTTGGTGTGTCTGACTCTCAAG 1378
Db 142 ProTyrProArgProGlyThrCysProSerLysThrPheGlyGlyPheAspSerThrLys 161
Qy 1379 GACCTTCTGATGTATTAACCTTTCGAAGAAGTATCCAGCCATGTATCAATCCAGTG 1438
Db 162 AspLeuProAspAspValIleThrPheAlaArgSerHisProAlaMetTyrAsnProVal 181
Qy 1439 TTTCTCTATGACAAATCCCAATAGTATCMAACCGATGTAATATCAATTTACAA 1498
Db 182 PheProMetAsnAsnArgProIleValIleLysThrAspValAsnTyrGlnPheThrGln 201
Qy 1499 ATTCTGCTAGACCGAGTGGATGAGAGATGACAGTATGATGTTATTCGGAACA 1558
Db 202 IleValValAspArgValAspAlaGluAspGlyGlnTyrAspValMetPheIleGlyThr 221
Qy 1559 GATCTTGGGACCGTCTTAACTAGTTCATTTCTTAAAGAGACTTGTATGATTTAGAA 1618
Db 222 AspValGlyThrValLeuLysValValSerIleProLysGluThrTyrPyrAspLeuGlu 241
Qy 1619 GAGTTCTGCTGGAAGAAATGACAGTGTTCGGGAACCGACTGCTATTTACGAATGGAG 1678
Db 242 GluValLeuLeuGluGluMetThrValPheArgGluProThrAlaIleSerAlaMetGlu 261
Qy 1679 CTTTCCACTAAGCAGCAGCACTATATATGTTTCAACGGCTGGGGTGGCCAGCTCCCT 1738
Db 262 LeuSerThrLysGlnGlnLeuTyrIleGlySerThrAlaGlyValAlaGlnLeuPro 281
Qy 1739 TTACACCGGTGTATATTTACGGGAAGCGTGTGCTGAGTGTGCTGCCCGAGACCT 1798
Db 282 LeuHisArgCysAspIleTyrGlyLysAlaCysAlaGluCysCysLeuAlaArgAspPro 301
Qy 1799 TACTGTCTTGGATGTTCTGCTGATGTTCTGCTATTTTCCACCTGCAAGAGAGCGACA 1858
Db 302 TyrCysAlaThrAspGlySerAlaCysSerArgTyrPheProThrAlaLysArgArgThr 321
Qy 1859 AGACGACAAGATATAAGAAATGGAGACCCACTGACTCTGCTGACACTTACACCATGAT 1918
Db 322 ArgArgGlnAspIleArgAsnGlyAspProLeuThrHisCysSerAspLeuHisAsp 341
Qy 1919 AATCACCATGCCACACCTGAGAGAGAACTATCTGTGTGAGAGATAGTAGCACA 1978
Db 342 AsnHisHisGlyHisSerProGluGluArgIleIleTyrGlyValGluAsnSerThr 361
Qy 1979 TTTTGGAAATGCAATCCGAAAGTCGAGAGAGCGCTGTCTATTTGGCAATTCAGAGCGGA 2038
Db 362 PheLeuGluCysSerProLysSerGlnArgAlaLeuValTyrTrpGlnPheGlnArg 381
Qy 2039 AATCAAGAGCGAAAGAGAGATCAGAGTGGATGATCATATCATCAGGACAGATCAAGC 2098
Db 382 AsnGluGluArgLysGluGluIleArgValAspAspHisIleIleArgThrAspGlnGly 401
Qy 2099 CTTCTGTACTAGTCTACAAACAGAGATTCAGGCAATTAATCTCTGCCATCGGTGGAA 2158
Db 402 LeuLeuLeuArgSerLeuGlnLysAspSerGlyAsnTyrLeuCysHisAlaValGlu 421
Qy 2159 CATGGTTCATCAAACTCTTCTTAAGGTAAACCTGGAAGTATTTGACGACAGAGCATTTG 2218

Db 422 HisGlyPheIleGlnThrLeuLeuLysValThrLeuGluValIleAspAsnGluHisLeu 441
Qy 2219 GAAGAACTTCTTCAATAAAGATGATGATGAGATGGCTCTTAAGACCAAGAAATGTCCAAT 2278
Db 442 GluGluLeuLeuHisLysAspAspGlyHisGlySerLysThrLysGluMetSerAsn 461
Qy 2279 AGCATCACACCTAGCCAGAAAGTCTGTACAGAGACTTCATCCAG 2323
Db 462 SerMetThrProSerGlnLysValTyrPyrArgAspPheMetGln 476
RESULT 9
US-09-308-179B-1
; Sequence 1, Application US/09308179B
; Patent No. 6436669
; GENERAL INFORMATION:
; APPLICANT: INAGAKI, Shinobu
; APPLICANT: FURUYAMA, Tatsuo
; TITLE OF INVENTION: NOVEL SEMAPHORIN GENES (I)
; FILE REFERENCE: 0020-4562P
; CURRENT APPLICATION NUMBER: US/09/308,179B
; CURRENT FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: PCT/JP97/04111
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: JAPAN 321068/1996
; PRIOR FILING DATE: 1996-11-15
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-308-179B-1
Alignment Scores:
Pred. No.: 3,09e-193 Length: 775
Score: 2030.00 Matches: 368
Percent Similarity: 67.75% Conservative: 155
Best Local Similarity: 47.67% Mismatches: 231
Query Match: 41.46% Indels: 18
Gaps: 8
US-09-774-490-1 (1-2709) x US-09-308-179B-1 (1-775)
Qy 218 ATGTCTGTCTTTCTGGGAGTATTACTTACAGCAAGCAAACTATCAGAATGGAG 277
Db 8 LeuThrLeuLeuLeuTrpGlyHisLeuLeuGluLeuTrpThrProGlyHisSerAlaAsn 27
Qy 278 AACAAATGTCGAAGCTCAAAATTTATCTACAAAGAAATGTTGGAATCCAAATGTGATC 337
Db 28 ProSerTyrProArgLeuArgLeuSerHisLysGluLeuLeuGluLeuAsnArgThrSer 47
Qy 338 ACTTTCATATGGCTTGGCCACAGCTCCAGTTATCATACCTTCTCTTTTGGATGGAGACGG 397
Db 48 IlePheGlnSerProLeuGlyPheLeuAspLeuHisThrMetLeuLeuAspGluTyrGln 67
Qy 398 ACTAGCTGTATGTGGAGCAAGAGATCACAATTTTTCATTCGACCTGGTTAATATCAAG 457
Db 68 GluArgLeuPheValGlyArgAspLeuValTyrSerLeuAsnLeuGluArgValSer 87
Qy 458 GAT---TTTCAAAGATGTTGTGGCCAGTATCTTACACCAAGAGAGATGAATGCAAGTGG 514
Db 88 AspGlyTyrArgGluIleTyrTrpProSerThrAlaValLysValGluGluCysIleMet 107
Qy 515 GCTGGAAGAGACATCCTGAAAGATGTCTAATTTTCAAGTACTTAAGGCATATAAT 574
Db 108 LysGlyLysAsp---AlaAsnGluCysAlaAsnTyrIleArgValLeuHisHisTyrAsn 126
Qy 575 CAGACTCACTTGTACCCCTGTGGAGCGGGCTTTTCATCCAAATTTGCACCTCATGTAA 634
Db 127 ArgThrHisLeuLeuThrCysAlaThrGlyAlaPheAspProHisCysAlaPheIleArg 146
Qy 635 ATTGGACATCATCTCTGAGGACATATTTTAAAGTGGAGAACTCACATTTTGAAGACGGC 694

Db 147 ValGlyHisSerGluGluProLeuPheHisLeuGluSerHisArgSerGluArgGly 166
QY 695 CGTGGGAAGAGTCATATACACCTAGCTGCTGACAGCATCCCTTTTATATAGATGGAGAA 754
Db 167 ArgGlyArgCysProPheAspProAsnSerSerPheValSerThrLeuValGlyAsnGlu 186
QY 755 TTATATCTCGGAACCTACGCTGATTTATGCGGCGAGACTTTGCTATCTCCGAACTCTT 814
Db 187 LeuPheAlaGlyLeuTyrSerAspTyrTrpGlyArgAspSerAlaIlePheArgSerMet 206
QY 815 GGCACACACCCACCAATCAGGACAGACAGCATGATTCAGAGTGGCTCAATGATCAAAAG 874
Db 207 GlyLeuLeuGlyHisIleArgThrGluHisAspAspGluArgLeuLeuGlySerProLys 226
QY 875 TTCATTAGTGGCCACCTCATCTCAGAGAGTGAACATCTCGTAGATCAACAACTATCTT 934
Db 227 PheValGlySerTyrMetIleProAspAsnGluAspArgAspAsnLysMetTyrPhe 246
QY 935 TTCCTCCGTGAAATCAATAGATGAGAACACTCTCGGAAAGACTACTCACCTAGAATA 994
Db 247 PhePheThrGluLysAlaLeuGluAlaGluAsnAlaHisThrIleTyrThrArgVal 266
QY 995 GGTACAGATATGCAAGAAATGACTTTGGAGGCGACAGAGTCTGGTGAATAAATGGACACA 1054
Db 267 GlyArgLeuCysValAsnAspMetGlyGlyGlnArgIleLeuValAsnLysTrpSerThr 286
QY 1055 TTCCTCAAGCTCGTCTGATTTGCTCAGTGGCAGGTCCTCAAAATGGCATTGACACTCATTT 1114
Db 287 PheLeuLysAlaArgLeuValCysSerValProGlyMetAsnGlyIleAspThrTyrPhe 306
QY 1115 GATGAACCTCAGAGATGATTTCTCAATGAACCTTAAAGATCCTAAATCCAGTTGTATAT 1174
Db 307 AspGluLeuGluAspValPheLeuLeuProThrArgAspProLysAsnProValIlePhe 326
QY 1175 GGAGTGTTCACGATCCAGTACATTTTCAAGGATCAGCGTGTGTATGATATAGCATG 1234
Db 327 GlyLeuPheAsnThrThrSerAsnIlePheArgGlyHisAlaValCysValTyrHisMet 346
QY 1235 AGTGTGTGAGAGGGTGTCTCTGTCATATGCCACAGGATGGACCCCAACTATCAA 1294
Db 347 SerSerIleArgGluAlaPheAsnGlyProTyrAlaHisLysGluGlyProGluTyrHis 366
QY 1295 TGGGTGCTTATCAGGAAGAGTCCCTATCCACGGCCAGAGAACTTGTCCGACGAAACA 1354
Db 367 TrpSerLeuTyrGluGlyLysValProTyrProArgProGlySerCysAlaSerLysVal 386
QY 1355 TTTGTGGT---TTTGACTCTCAAAAGGACCTTCTGATGATGTTATACCTTTGCAAGA 1411
Db 387 AsnGlyGlyLysTyrGlyThrThrLysAspTyrProAspAspAlaIleArgPheAlaArg 406
QY 1412 AGTCATCCAGCATGTACAAATCCAGTTTCCATGAACAATCGCCCAATAGTATCAAA 1471
Db 407 MetHisProLeuMetTyrGlnProIleLysProValHisLysLysProIleLeuValLys 426
QY 1472 ACGGATGTAAATCAATTTACAAATTTGCTGATAGCCGAGTGGATGCGAGATGGA 1531
Db 427 ThrAspGlyLysTyrAsnLeuArgGlnLeuAlaValAspArgValGluAlaGluAspGly 446
QY 1532 CAGTATGATGTTATGTTATCGGAACAGATGTGGGCGCTTCTTAAAGTAGTATCAATT 1591
Db 447 GlnTyrAspValLeuPheIleGlyThrAspThrGlyIleValLeuLysValIleThrIle 466
QY 1592 CTAAGGAGACTGGTATGATTAAGAGAGTTCGCTGGGAAGAAATGACAGTATTTCCG 1651
Db 467 TyrAsnGlnGluThrGluTrpMetGluGluValIleLeuGluGluLeuGlnIlePheLys 486
QY 1652 GAACGACGCTGATTTACAGATGGAGCTTCCATTAAGCAGCAACAATATATATTCGT 1711
Db 487 AspProAlaProIleSerMetGluIleSerSerLysArgGlnLeuTyrIleGly 506
QY 1712 TCAACGCTGGGTGCGCCAGCTCCCTTTACACCGGTGTGATTTACGGGAAACGCGT 1771
Db 507 SerAlaSerAlaValAlaGlnValArgPheHisCysAspMetTyrGlySerAlaCys 526

QY 1772 GCTGAGTGTTCCTCGCCGAGACCCCTTACTGTCTTTGGGATGTTCTGCTATGTTCTCGC 1831
Db 527 AlaAspCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlyIleSerCysSerArg 546
QY 1832 TATTTTCCCACT-----GCAAGAGACGACACAGACACAGATATAAGAAATGGA 1882
Db 547 TyrTyrProThrGlyAlaHisAlaLysArgPheArgGlnAspValArgHisGly 566
QY 1883 GACCACTGACTCATCTGTTCCAGACTTACACCATGATAATCACCATGCGCCACAGCCCTGAA 1942
Db 567 AsnAlaAlaGlnGlnCysPheGlyGlnGlnPheValGlyAspAlaLeuAspArgThrGlu 586
QY 1943 GAGAGATCATCTATGTGTAGAGATAGTAGACATTTTGGATCCAGCTCCGAATCG 2002
Db 587 GluArgLeuAlaTyrGlyIleGluSerAsnSerThrLeuLeuGluCysThrProArgSer 606
QY 2003 CAGAGAGCGTGTCTATTGCAATTCAGAGCGGCAATGAAGAGCGCAAAAGAGAGATC 2062
Db 607 LeuGlnAlaLysValIleTyrPheValGlnLysGlyArgAspValArgLysGluGluVal 626
QY 2063 AGAGTGTATGATCATATCATCAGACAGATCAAGGCCTTCTGTACTGTACTGTACACAG 2122
Db 627 LysThrAspAspArgValValLysMetAspLeuGlyLeuLeuPheLeuArgValArgLys 646
QY 2123 AAGGATTGAGCAATTAACCTCTGCTGCGTGGACATCGGTTTCATACAACTCTTCTT 2182
Db 647 SerAspAlaGlyThrTyrPheCysGlnThrValGluHisAsnPheValHisThrValArg 666
QY 2183 AAGTAAACCTTGGAGTCTATTGACACAGACATTTGGAAGAACTTCTTATAAAGATGAT 2242
Db 667 LysIleThrLeuGluValValGluGluHisLysValGluGlyMetPheHisLysAspHis 686
QY 2243 GATGGAGATGGCTCTAGACCAAGAATGTCC-----AATACATGACACCT 2290
Db 687 GluGluGlu-----ArgHisLysMetProCysProLeuSerGlyMetSerGln 704
QY 2291 AGCCAGAGAGTCTGGTACAGAGACTTCATGACGCTCATCAACCAACCAATCTCAACACG 2350
Db 705 GlyThrLysProTyrTyrLysGluPheLeuGlnLeuIleGlyTyrSerAsnPheGlnArg 724
QY 2351 ATGATGAGTCTGTGAACAAGTTTGAAGAAGGACCGCAAAACAACGTCGGCAAGGCCA 2410
Db 725 ValGluGluTyrCysGluLysValTyrCysThrAspLysLysArgLysLysLeuLysMet 744
QY 2411 GGACATACCCAGGGAACAGTAAACAATGGAACACTTACAGAAATAAGAAAGGTAGA 2470
Db 745 -----SerProSerLysTyrLysTyrAlaAsnProGlnGluLys---Arg 758
QY 2471 AACAGGAGACCCACGAAATTTGAGAGGCGCACCCAGG 2506
Db 759 LeuArgSerLysAlaGluHisPheArgLeuProArg 770

RESULT 10

US-08-556-422A-2
; Sequence 2, Application US/08556422A
; Patent No. 6576754
; GENERAL INFORMATION:
; APPLICANT: HALL, Kathryn T.
; APPLICANT: FREEMAN, Gordon J.
; APPLICANT: SCHULTZE, Joachim L.
; APPLICANT: BOUSSETIOTIS, Vassiliki
; APPLICANT: NADLER, Lee M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING CD100 MOLECULES
; FILE REFERENCE: DFN-005CPA2
; CURRENT APPLICATION NUMBER: US/08/556,422A
; CURRENT FILING DATE: 1995-11-09
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 862
; TYPE: PRT
; ORGANISM: Homo sapiens

US-08-556-422A-2

Alignment Scores:

Pred. No.:

Score:

Percent Similarit

Best Local Similarity

Query Match:

DB:

Length: 862

Matches: 246

Conservative: 115

Mismatches: 218

Indels: 123

Gaps: 26

22A-2 (1-862)

AAAGAAATGTTGGAATCCA

.....

ArgGluVal-----

US-09-774-490-1 (1-2709) x US-08-556-422A-2 (1-862)

284	GTGCCAAGCGCTGAATAATTATCTCTCAAAAGAAATGTTGGAATCCCAACAATGTGATCACTTTC	343
QY		
27	ileProArgIleThrTpGluHisArgGluVal-----HisIeuValGlnPhe	42
DB		
344	AATGCTTTGGCCAAACAGCTCCAGCTTATCATACCTTCCTTTTGATGAGGAACGGAGTAGG	403
QY		
43	HisGlu---ProAspIleTyrAsnTyrSerAlaLeuLeuLeuSerGluAspLysAspThr	61
DB		
404	CTGTATGTTGGAGCAAGGATCACATATTTTCATTTCAGCTGGTATTAATATCAAGATTTT	463
QY		
62	LeuTyrIleGlyAlaArgGluAlaValPheAlaValAsnAlaLeuAsnIleSerGluLys	81
DB		
464	CAA---AAGATTGTGTGCCCATGTATCTTACACAGAGAGAGATCAATGCAAGTGGCGCTCGA	520
QY		
82	GlnHisGluValTyrTpLysValSerGluAspLysLysAlaLysCysAlaGluLysGly	101
DB		
521	AAAGACATCTGAAAGATGTGCTAAATTTCATCAAGGTACTTAAGGCATATATATCAGACT	580
QY		
102	LysSerLysGlnThrGluCysLeuAsnTyrIleArgValLeuGlnProLeuSerAlaThr	121
DB		
581	CACTTGTACGCGCTGTGAACGGGGCGCTTTTCATCCAATTTGCACCTACATTCAAATTCGA	640
QY		
122	SerLeuTyrValCysGlyThrAsnAlaPheGlnProAlaCysAspHisLeuAsnLeu---	140
DB		
641	CATCATCTCGAGGACAATATTTTAAAGTCGAGAACTCACATTTGAAAACGGCGCTGGG	700
QY		
141	-----ThrSerPheLysPheLeuGlyLysAsn---GluAspGlyLysGly	154
DB		
701	AAGATCCCATATGACCTTAAGCTGTGACAGCATCCCTTTTAAATAGATGGAGAATTAPAC	760
QY		
155	ArgCysProPheAspProAlaHisSerTyrThrSerValMetValAspGlyLeuTyr	174
DB		
761	TCGTGAACCTCGAGCTGATTTATGGGGCGAGACTTTCCTATCTCCGAACCTCTGGGCAC	820
QY		
175	SerGlyThrSerTyrAsnPheLeuGlySerGluProIleIleSerArgAsn---SerSer	193
DB		
821	CACCAACCAATCAGACAGACAGCATGATTCAGGTGGCTCAATGATCCAAAGTTCATT	880
QY		
194	HisSerProLeuArgThrGlu---TyrAlaIleProTyrLeuAsnGlnProSerPheVal	212
DB		
881	AGTGGCCACCCATCTCAGAGAGT---GACAATCCT-----GAAGATGACAAAGATATAC	931
QY		
213	PheAlaAspValIleArgLysSerProAspSerProAspGlyGluAspArgValTyr	232
DB		
932	TTTTCTTCCTGGGAATGCAATAGATGGAGACACTCTGGAAAAGCTACTCAAGCTAGA	991
QY		
233	PhePhePheThrGluValSerValGluTyrGluPheValPheArgValLeuIleProArg	252
DB		
992	ATAGTCAGATATCAAGAATGACTTTGGAGGGCACAGAAGTCTGGTAATAAATGGACA	1051
QY		
253	IleAlaArgValCysLysGlyAspGlnGlyLeuArgThrLeuGlnLysIleTyrThr	272
DB		
1052	ACATTTCCFCAAAGCTCGCTGANTTGTCTAGTCCGACAGTCCAAATGGCATGACACTCAT	1111
QY		
273	SerPheLeuLysAlaArgLeuIleCysSerArgProAspSerGlyLeuVal-----	289
DB		
1112	TTTGATGAACCTGCAAGGATGATTCTCTTAATGAACCTTAAAGATCCTAAATAACGATGCTA	1171
QY		
290	PheAsnValLeuArgAspValPheValLeuArgSerProGlyLeuLysValProValPhe	309
DB		
1172	TATGAGTGTTTACGACTCCAGTAACATTTTCAAGGGATCAGCGCTGTGTATGTATAGC	1231
QY		

Db 623 GlnCysLeuSerGluGluArgValLysAsnLysThrValPheGlnValValAlaLysHis 642
 QY 2189 -----ACCTGGAAGTCATTGAC 2206
 Db 643 ValLeuGluValLysValValProLysProValValAlaProThrLeuSerValValGln 662
 QY 2207 ACAGAG 2212
 Db 663 ThrGlu 664

RESULT 11

US-08-556-422A-4
 ; Sequence 4, Application US/08556422A
 ; Patent No. 6576754
 ; GENERAL INFORMATION:
 ; APPLICANT: HALL, Kathryn T.
 ; APPLICANT: FREEMAN, Gordon J.
 ; APPLICANT: SCHEUTZ, Joachim L.
 ; APPLICANT: BOUSSIOPTIS, Vassiliki
 ; APPLICANT: NADLER, Lee M.
 ; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING CD100 MOLECULES
 ; FILE REFERENCE: DFN-005CPA2
 ; CURRENT APPLICATION NUMBER: US/08/556,422A
 ; CURRENT FILING DATE: 1995-11-09
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 607
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 ; US-08-556-422A-4

Alignment Scores:
 Pred. No.: 1,45E-74 Length: 607
 Score: 838.50 Matches: 210
 Percent Similarity: 49.84% Conservative: 106
 Best Local Similarity: 33.12% Mismatches: 249
 Query Match: 17.13% Indels: 69
 DB: 4 Gaps: 22

US-09-774-490-1 (1-2709) x US-08-556-422A-4 (1-607)

QY 356 AACAGCTCAGTATCATACCTCTCTTTGGATGAGGACGAGTAGGCTGTATGTTGA 415
 Db 12 AshLLeuSerAsnLysThrAlaLeuLeuSerGlnAspGlyLysThrLeuTyrValGly 31
 QY 416 GCAAGAGTCACATATTTTCATTCGACCTGGTGTATATCAAG-----GAT 460
 Db 32 AlaArgGluAlaLeuPheAlaLeuAsn---SerAsnLeuSerPheLeuProGlyGlyGlu 50
 QY 461 TTTCAAGAGTTGTGTGGCCAGTATCTTACACGACGAGATGAATGCAAGTGGCTGGA 520
 Db 51 TyrGlnGluLeuLeuTrpSerAlaAspAlaAspArgLysGlnGlnCysSerPheLysGly 70
 QY 521 AAAGACATCCTGAAGAATGCTATTTTCATCAAGGTACTTAAGGCATATAATCAGACT 580
 Db 71 LysAspProLysArgAspCysGlnAsnLysLysLeuLeuProLeuAsnSerSer 90
 QY 581 CACTGTGACGCTGTGGAACGGGGCTTTTCACAAATTTGCACATTCACATTGAATGGA 640
 Db 91 HisLeuLeuThrCysGlyThrAlaAlaPheSerProLeuCysAlaTyrIleHisIleAla 110
 QY 641 CATCATCTCGAGACATATTTTAAAGCTGGAG-----AACTCACATTTT 685
 Db 111 Ser-----PheThrLeuAlaGlnAspGluAlaGlyAsnValIleLeu 124
 QY 686 GAAACGGCGGTGGGAAGAGTCCATATGACCTTAAGCTGCTGACAGCATCCCTTTTAATA 745
 Db 125 GluAspGlyLysGlyHisCysProPheAspProAsnPheLysSerThrAlaLeuValVal 144
 QY 746 GATGGAGATTATCTGGAACGAGCTGATTTTATGGGCGGAGACTTTGCTATCTTC 805
 Db 145 AspGlyGluLeuTyrThrGlyThrValSerSerPheGlnGlyAsnAspProAlaIleSer 164

QY 806 CGAACTCTTGGGACACACCAATCAGACGACGACGATGATTCACGGTGGCTCAAT 865
 Db 165 ArgSerGlnSer---SerArgProThrLysThrGluSer---SerLeuAsnTrpLeuGln 162
 QY 866 GATCAAAAGTTCAATTAGTGCCACCTCATCTCAGAGAGT---GACATCTCT---GAA 916
 Db 183 AspProAlaPheValAlaSerAlaThrSerProGluSerLeuGlySerProIleGlyAsp 202
 QY 917 GATGACAAAGTATATCTTTTCTCCGTGAAAAATGCAATAGATGAGAGACACTCTGGAAA 976
 Db 203 AspAspLysIleTyrPhePheSerGluThrGlyGlnGluPheGluPheGluAsn 222
 QY 977 GCTACTCACGCTAGATAGGTGAGATGCAAGATGACTTTGGAGGGCACAGAGCTG 1036
 Db 223 ThrIleValSerArgValAlaArgValCysLysGlyAspGluGlyGluArgValLeu 242
 QY 1037 GTGAATAAATGGACAACATCTCTCAAGTCGTGATTTGCTCAGTCGACGTCCTCAAT 1096
 Db 243 GlnGlnArgTrpThrSerPheLeuLysAlaGlnLeuLysCysSerArgPro---AspAsp 261
 QY 1097 GGCATTGACACTCATTTTGTATGAACGAGGATGATTCCTAATG-----AACTTTAA 1150
 Db 262 GlyPhePro-----PheAsnValLeuGlnAspValPheThrLeuAsnProAsnProGln 279
 QY 1151 GATCCTAAAAATCCAGTTGTATGAGTGTTCACGACTTC-----AGTAACATTTTC 1204
 Db 280 AspTrpArgLysThrLeuSerIleGlyValPheThrSerGlnTrpHisArgGlyThrThr 299
 QY 1205 AAGGATCAGCGTGTATGTATAGCATGATGATGATGAGAGGGTGTCTTCTGTGTTCA 1264
 Db 300 GluGlySerAlaIleCysValPheThrMetAsnAspValGlnLysAlaPheAspGlyLeu 319
 QY 1265 TATGCCACAGGATGAGCAACTATCAATGGTGTCTTATCAAGAGAGTCCCTAT 1324
 Db 320 TyrLysLysValAsnArgGluThrGlnGlnTrpTyrThrGluThrHisGlnValProThr 339
 QY 1325 CCACGGCCAGAACTTGT-----CCACGAAACATTTGGTGGTTGACTCTCAAG 1378
 Db 340 ProArgProGlyAlaCysIleThrAsnSerAlaArgGluArgLysIleAsnSerSerLeu 359
 QY 1379 GACCTTCCTGATGATGATATACCTTTTGCAGAGATCATCCAGCATGTACATCCAGTG 1438
 Db 360 GlnLeuProAspArgValLeuAsnPheLeuLysAspHisPheLeuMetAspGlyGlnVal 379
 QY 1439 TTTCTATGAACATCGCCCAATAGTATCAAAACGAGTGTAAATTTATCAATTTACACAA 1498
 Db 380 -----ArgSerArgLeuLeuLeuGlnProArgAlaArgTyrGln-----Arg 394
 QY 1499 ATTGTCGTACACGAGTGGATGACAGAGATGGACAGTATGATGTTATGTTATCGGAACA 1558
 Db 395 ValAlaValHisArgValProGlyLeuHisSerThrTyrAspValLeuPheLeuGlyThr 414
 QY 1559 GATGTTGGGACCGTCTTAAAGTAGTTTCAATTCCTAAGGAGACTTGGTATGATTTAGAA 1618
 Db 415 GlyAspGlyArgLeuHisLysAlaValThrLeuSerSerArgValHis-----430
 QY 1619 GAGTTCTGCTGGAAGAAATGACAGTTTTTCGGGAACCGACTCTCTATTTTTCAGCAATGGAG 1678
 Db 431 -----IleIleGluGluLeuGlnIlePheProGlnGlyGlnProValGlnAsnLeuLeu 448
 QY 1679 CTTTCCACTAAGCAGCAACACTATATATTGGTTCAACGGCTGGGGTGGCCAGCTCCCT 1738
 Db 449 LeuAspSerHisGlyGlyLeuLeuTyrAlaSerSerHisSerGlyValValGlnValPro 468
 QY 1739 TTACACCGGTGTATTTTACGGGAAAGCGTGTGCTGAGTGTTCCTCGCCCGACACCTT 1798
 Db 469 ValAlaAsnCysSerLeuTyr---ProThrCysGlyAspCysLeuLeuAlaArgAspPro 487
 QY 1799 TACTGTCTTGGATGTTCTGCTGCTG-----TCTGCTATTTTCCACTGCAAG 1849
 Db 488 TyrCysAlaTrpThrGlySerAlaCysArgLeuAlaSerLeuTyrGlnProAspLeuAla 507

QY 1850 AGAGCCACAGACAGACAGATATAGAAATGGAGACCCACTGACTCTACTTCCAGACTTA 1909
 Db |||||
 508 SerArgProTptThrGlnAspIleGluGlyAlaSerValLysGluLeuCysLysAsn-- 526
 QY 1910 CACCATGATATACCATGGCCACAGCCCTCAAGAGAGATCATCTATGCTGTAGAG-- 1966
 Db |||||
 527 -----SerSerTyrLysAlaArgPheLeuValProGlyLysPro 539
 QY 1967 -----AATAGTAGCACATTTTGGAAATCCAGTCCGAAGTGG 2002
 Db |||||
 540 CysLysGlnValGlnIleGlnProAsnThrValAsnThrLeuAlaCysProLeuLeuSer 559
 QY 2003 CAGAGAGCGCTGCTGCTATGTCGAATTCAGAGGCGAATGAGAGCGAAAGAGAGATC 2062
 Db |||||
 560 AsnLeuAlaThrArgLeuTrpValHisAsnGlyAlaProValAsnAlaSerAlaSerCys 579
 QY 2063 AGAGTGGGATGATCATATCATCAGGACAGATCAAGGCGCTTCTGCTACGTAGTCTACACAG 2122
 Db |||||
 580 ArgVal-----LeuProThrGlyAspLeuLeuValGlySer-----Gln 593
 QY 2123 AAGGATCAGCAATTAATCTCTGCGATCGGTGGAGCATGGG 2164
 Db |||||
 594 GlnGlyLeuGlyValPheGlnCysTrpSerIleGluGly 607

RESULT 12

US-09-653-274-8
 ; Sequence 8, Application US/09653274
 ; Patent No. 6635742

GENERAL INFORMATION:
 ; APPLICANT: Boyle, Bryan J
 ; APPLICANT: Yeung, George Y
 ; APPLICANT: Arterburn, Matthew C
 ; APPLICANT: Mize, Nancy K
 ; APPLICANT: Tang, Y. Tom
 ; APPLICANT: Liu, Chenghua
 ; APPLICANT: Drmanac, Radoje T
 ; TITLE OF INVENTION: Methods and Materials Relating to Semaphorin-Like
 ; TITLE OF INVENTION: Polypeptides and Polynucleotides
 ; FILE REFERENCE: HYS-23

CURRENT APPLICATION NUMBER: US/09/653,274

CURRENT FILING DATE: 2000-08-31

PRIOR APPLICATION NUMBER: 09/491,404

PRIOR FILING DATE: 2000-01-10

NUMBER OF SEQ ID NOS: 13

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 8

LENGTH: 1070

TYPE: PRT

ORGANISM: Homo sapiens

US-09-653-274-8

Alignment Scores:
 Pred. No.: 2,73e-72 Length: 1070
 Score: 817.00 Matches: 206
 Percent Similarity: 47.54% Conservative: 113
 Best Local Similarity: 30.70% Mismatches: 233
 Query Match: 16.69% Indels: 119
 DB: 4 Gaps: 25

US-09-774-490-1 (1-2709) x US-09-653-274-8 (1-1070)

QY 353 GCCAACAGTCCAGTATCATACCTTC-----CTTTGGATGAGGACGGAGTAGG 403
 Db |||||
 33 SerGlyAsnGluSerGlnHisArgLeuAspPheGlnLeuMetLeuLysIleArgAspThr 52
 QY 404 CTGTATGTTGGACCAAGATGATCATATTTTTCATTCGACCTCGTGAATATCAAGATTTT 463
 Db |||||
 53 LeuTyrIleAlaGlyArgAspGlnValTyrThr-----ValAsnLeuAsnGluMet 69
 QY 464 -----CAAAAGATTGTGGCCAGTATCTTACACAGAGA 499
 Db |||||
 70 ProLysThrGluValIleProAsnLysLysLeuThrTrpArgSerArgGlnAspArg 89

QY 500 GATGAATCGAGTGGCGTGGAAAGACATCTCTGAAAGAAATGTGCTAAATTTTCATCAAGTA 559
 Db |||||
 90 GluAsnCysAlaMetLysGlyLysHis---LysAspGluCysHisAsnPheIleLysVal 108
 QY 560 CTTAAGGATATAATACAGACTCATCTGTACGCTGTGGAAACGGGGCTTTTCATCCAATT 619
 Db |||||
 109 PheValProArgAsnAspGluMetValPheValCysGlyThrAsnAlaPheAsnProMet 128
 QY 620 TGCACCTACATTTGAATTTGGACATCATCTCTGAGGACATATTTTAACTCGAGAACTCA 679
 Db |||||
 129 CysArgTyr-----TyrArgLeuSerThrLeu 137
 QY 680 CATTTTTGA-----AACGGCGTGGGAGAGTCCATATGACCCCTAAGCTGCTG 727
 Db |||||
 138 GluTyrAspGlyGluGluIleSerGlyLeuAlaArgCysProPheAspAlaArgIleThr 157
 QY 728 ACAGCATCCCTTTTAAATAGATGGAGAATATATCTCTGGAAGTGCAGCTGATTTTATGGG 787
 Db |||||
 158 AsnValAlaLeuPheAlaAspGlyLysLeuTyrSerAlaThrValAlaAspPheLeuAla 177
 QY 788 CGAGACTTTTGTCTATCTCTCGAACTCTTGGGACCAACCAATCAGGACAGAGCAT 847
 Db |||||
 178 SerAspAlaValIleTyrArgSerMetGlyAspGlySerAlaLeuArgThrIleLysTyr 197
 QY 848 GATTCAGGTGCTCAATGATCCAAAGTTTCATTAGTGCCTCCACCTCATCTCAGAGAGTGC 907
 Db |||||
 198 AspSerLysTrpIleLysGluProHisPheLeu-----HisAlaIleGluTyrGly--- 214
 QY 908 AATCTCGAAGATGACAAAGTATCTTTTCTCCGTGAAATGCAATAGATGGAGAACAC 967
 Db |||||
 215 -----AsnTyrValTyrPhePheArgGluIleAlaValGluHisAsnAsn 230
 QY 968 TCTGAAAAAGTACTACGCTAGATAGATAGATGCAAGATGCAAGATGCTTTGGAGGAC 1027
 Db |||||
 231 LeuGlyLysAlaValTyrSerArgValAlaArgGlyLysAsnAspMetGlyLys 250
 QY 1028 AGAAGTCTGGTGAATAA---TGGACACATCTCCAAAGCTCGTCTGATTTGCTCAGTG 1084
 Db |||||
 251 GlnArgValLeuGluLysHisTrpThrSerPheLeuLysAlaArgLeuAsnCysSerVal 270
 QY 1085 CCAGGTCCAAATGGCATTCATCTGATGTAAGTGCAG-----GATCATTC 1135
 Db |||||
 271 ProGlyAspProPhePhe-----TyrPheAspValLeuGlnSerIleThrAspIle 288
 QY 1136 CTAATGAACCTTAAAGATCCTAAATCCAGTGTATATGAGTCTGTTACGACTTCCAGT 1195
 Db |||||
 289 GlnIleAsn-----GlyIleProThrValValGlyValPheThrThrGlnLeu 304
 QY 1196 AACATTTTCAAGGATCAGCGTGTATGTATGATGATGATGATGATGATGATGATGATGATG 1255
 Db |||||
 305 AsnSerIleProGlySerAlaValCysAlaPheSerMetAspAspIleGluLysValPhe 324
 QY 1256 CTTGGTCCATATGCCCAAGGATGGACCAACTATCAATGG-----GTGCTTATCAA 1309
 Db |||||
 325 LysGlyArgPheLysGluGlnLysThrProAspSerValTrpThrAlaValPro---Glu 343
 QY 1310 GGAAGAGTCCCTTATCCAGCGCCAGGAACTTGTGCCAGCAAAACATTTGGT---GTTT 1366
 Db |||||
 344 AspLysValProLysProArgProGlyCysCysAlaLysHisGlyLeuAlaGluAlaTyr 363
 QY 1367 GACTTACAAAGGACCTTCTGATGATGATTAACCTTTGCAAGAGTATCATCCAGCATG 1426
 Db |||||
 364 LysThrSerIleAspPheProAspGluThrLeuSerPheIleLysSerHisProLeuMet 383
 QY 1427 TACATCCAGTCTTCTATGACATGCCCAATAGTATGATCAAAACGATGTAATAT 1486
 Db |||||
 384 AspSerAlaValProIleAlaAspGluProTrpPheThrLysThrArgValArgTyr 403
 QY 1487 CAATTACAAATTTGCTGTAGACCGAGTGGATGCAAGAGATGGACAGATGATGATGATG 1546
 Db |||||
 404 ArgLeuThrAlaIleSerValAspHisSerAlaGlyProTyrGlnAsnTyrThrValIle 423
 QY 1547 TTTATCGGAACAGATGTTGGACCGTCTCTTAAAGTAGTTTCAATTCCTTAAGGAGACTGG 1606

QY 788 CGAGACTTTGCTATCTTCGCACTCTGGCCACCACCACCCCAATCAGGACAGCAGCAT 847
 Db 178 SerAspAlaValIleTyrArgSerMetGlyAspGlySerAlaLeuArgThrIleLysTyr 197
 QY 848 GATTCAGGTGGCTCAATGATCAAAAGTTCAATAGTCCCACTCATCTCCAGAGAGTGAC 907
 Db 198 AspSerLysTrpIleLysGluProHisPheLeu-----HisAlaIleGluTyrGly--- 214
 QY 906 AATCCTGAGATGACAAAGATATATCTTTCTTCGTAAGAAATGCAATAGATGAGAGAAC 967
 Db 215 -----AsnTyrValTyrPhePhePheArgGluIleAlaValGluHisAsnAsn 230
 QY 968 TCTGAAAAGCTACTCAGCTAGATAGTTCAGATATGCAAGAAATGACTTTTCGAGGGCAC 1027
 Db 231 LeuGlyLysAlaValTyrSerArgValAlaArgIleCysLysAsnAspMetGlyGlySer 250
 QY 1028 AGAAGTCTGGTGNATAAA---TGGACAATCTCTCAAGCTCGCTGATTTGCTCAGTG 1084
 Db 251 GlnArgValLeuGluLysHisTrpThrSerPheLeuLysAlaArgLeuAsnCysSerVal 270
 QY 1085 CCAGGTCCAAATGGCATTGACACTCATTTTGTGATGAATCGAG-----CATGTATTC 1135
 Db 271 ProGlyAspProPhePhe-----TyrPheAspValLeuGlnSerIleThrAspIlele 288
 QY 1136 CTAATGAATTTAAGATCCTAAATCCAGTTGTATGATGGAGTGTTCACGACTTCCAGT 1195
 Db 289 GlnIleAsn-----GlyIleProThrValValGlyValPheThrThrGlnLeu 304
 QY 1196 AACATTTTCAAGGATCAGCGGTGTATGTATGATGATGATGATGATGATGATGATGATG 1255
 Db 305 AsnSerIleProGlySerAlaValCysAlaPheSerMetAspAspIleGluLysValPhe 324
 QY 1256 CTGTGTCCTATATGCCAGGATGACCCCAATCATATCATG-----GTGCTTATCAA 1309
 Db 325 LysGlyArgPheLysGluGlnLysThrProAspSerValTrpThrAlaValPro---Glu 343
 QY 1310 GGAAGAGTCCCTATCCAGCGCAGGAATCTGTCAGCAAAACATTTGGT---GGTTTT 1366
 Db 344 AspLysValProLysProArgProGlyCysAlaLysHisGlyLeuAlaGluAlaTyr 363
 QY 1367 GACTCTACAAAGACCTCTCTGATGATGTTATAACCTTTGCAAGAGTCAATCCAGCCCATG 1426
 Db 364 LysThrSerIleAspPheProaspGluThrLeuSerPheIleLysSerHisProLeuMet 383
 QY 1427 TCAATCCAGTGTTCCTATGAAACAAATCCCAATAGTATGATCAAAACGGATGTAATAT 1486
 Db 384 AspSerAlaValProProIleAlaAspGluProTyrPheThrLysThrArgValArgTyr 403
 QY 1487 CAATTTACACAATCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1546
 Db 404 ArgLeuThrAlaIleSerValAspHisSerAlaGlyProTyrGlnAsnTyrThrValIle 423
 QY 1547 TTTATCGGAACAGATGTTGGGACCGTCTTAAAGTAGTTTCAATTCCTAAGAGACTTGG 1606
 Db 424 PheValGlySerGluAlaGlyMetValLeuLysValLeuAla-----LysThrSerPro 441
 QY 1607 TATGATTTA---GAAGAGTGTCTGCGAGAAATGACAGTTTTT----- 1648
 Db 442 PheSerLeuAsnAspSerValLeuLeuGluGluIleGluAlaTyrAsnHisAlaLysCys 461
 QY 1649 -----CGGGAACCGACTGCTATTTCAGCAATGGAGCTTTCACCTAAGCAGCAA 1696
 Db 462 SerAlaGluAsnGluAspLysLysValIleSerLeuGlnLeuAspLysAspHis 481
 QY 1697 CAACTATATTTGGTTCAACGGCTGGGTGGTCCAGCTCCCTTTACACGGTGTATAT 1756
 Db 482 AlaLeuTyrValAlaPheSerSerCysIleIleArgIleProLeuSerArgCysGluArg 501
 QY 1757 TACGGGAAGCGTGTGCTGAGTGTGCTCGCCCGAGACCTTACTGTGCTGG---CAT 1813
 Db 502 TyrGlySerCysLysLysSerCysIleAlaSerArgAspProTyrCysGlyTrpLeuSer 521

QY 1814 GGTTCTGCATGTTCTCGTATTTTCCACTGCAAGAGACGACCAAGA----- 1851
 Db 522 GlnGlySerCysGlyArgValThrProGlyMetLeuLeuThrGluAspPhePheAla 541
 QY 1862 -----CGACAAGATATAAGAAATGAGAGACCCACTGACT 1894
 Db 542 PheHisAsnHisSerAlaGluGlyTyrGluGlnAspThrGluPheGlyAsn---ThrAla 560
 QY 1895 CACTGTTTCAGACTTACACCATGATAATCACCATGCCACACCCCTGAGAGAGATCATC 1954
 Db 561 HisLeuGlyAspCysHisGluIleLeuProThrSerThrProAspTyrLysIlePhe 580
 QY 1955 TATGGT-----GTAGAGAATAGTACGACATTT 1981
 Db 581 GlyGlyProThrSerAspMetGluValSerSerSerValThrThrMetAlaSerIle 600
 QY 1982 TTGGAATGCGACTCCGAAG 1999
 Db 601 ProGluIleThrProLys 606
 RESULT 15
 US-08-121-713D-62
 ; Sequence 62, Application US/08121713D
 ; Patent No. 5639856
 ; GENERAL INFORMATION:
 ; APPLICANT: Goodman, Corey S.
 ; APPLICANT: Kolodkin, Alex L.
 ; APPLICANT: Matthes, David
 ; APPLICANT: Bentley, David R.
 ; APPLICANT: O'Connor, Timothy
 ; TITLE OF INVENTION: The Semaphorin Gene Family
 ; NUMBER OF SEQUENCES: 100
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
 ; STREET: 268 Bush Street, Suite 3200
 ; CITY: San Francisco
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94104
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/121,713D
 ; FILING DATE: 13-SEP-1993
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Osman, Richard A.
 ; REGISTRATION NUMBER: 36,627
 ; REFERENCE/DOCKET NUMBER: B94-002-1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415)343-4341
 ; TELEFAX: (415) 343-4342
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 62:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 724 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-121-713D-62
 Alignment Scores:
 Pred. No.: 3,04e-69 Length: 724
 Score: 785.50 Matches: 221
 Percent Similarity: 47.48% Conservative: 118
 Best Local Similarity: 30.95% Mismatches: 248
 Query Match: 16.04% Indels: 127
 DB: 1 Gaps: 30
 US-09-774-490-1 (1-2709) x US-08-121-713D-62 (1-724)

Search completed: September 21, 2004, 19:50:37
Job time : 116.5 secs

This Page Blank (uspio)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 23, 2004, 01:19:05 ; Search time 1239 Seconds
(without alignments)
11035.942 Million cell updates/sec

Title: US-09-774-490-1

Perfect score: 2709
Sequence: 1 aatctttattttatcgatg.....aggcttttttctaatacc 2709

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3327077 seqs, 2523723180 residues

Total number of hits satisfying chosen parameters: 6654154

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
- 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
- 18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
- 19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2709	100.0	2709	9	US-09-774-490-1
2	2517	92.9	2848	15	US-10-247-671-83
3	2508.4	92.6	2530	15	US-10-037-340-283
4	2508.4	92.6	2530	15	US-10-262-538-9
5	2508.4	92.6	2601	15	US-10-067-632-53
6	718.6	26.5	2331	16	US-10-404-438-2
7	718.6	26.5	3871	10	US-09-946-374-309
8	718.6	26.5	3871	12	US-10-015-395A-309
9	718.6	26.5	3871	13	US-10-206-915-347
10	718.6	26.5	3871	13	US-10-199-670-347
11	718.6	26.5	3871	13	US-10-201-858-347
12	718.6	26.5	3871	13	US-10-205-890-347
13	718.6	26.5	3871	13	US-10-208-024-347
14	718.6	26.5	3871	13	US-10-201-853-347

15	718.6	26.5	3871	13	US-10-174-581-347	Sequence 347, App
16	718.6	26.5	3871	13	US-10-176-483-347	Sequence 347, App
17	718.6	26.5	3871	13	US-10-176-749-347	Sequence 347, App
18	718.6	26.5	3871	13	US-10-176-914-347	Sequence 347, App
19	718.6	26.5	3871	13	US-10-176-915-347	Sequence 347, App
20	718.6	26.5	3871	13	US-10-006-485A-309	Sequence 309, App
21	718.6	26.5	3871	13	US-10-013-907A-309	Sequence 309, App
22	718.6	26.5	3871	13	US-10-015-499A-309	Sequence 309, App
23	718.6	26.5	3871	13	US-10-176-484-347	Sequence 347, App
24	718.6	26.5	3871	13	US-10-180-550-347	Sequence 347, App
25	718.6	26.5	3871	13	US-10-183-014-347	Sequence 347, App
26	718.6	26.5	3871	13	US-10-187-738-347	Sequence 347, App
27	718.6	26.5	3871	13	US-10-187-740-347	Sequence 347, App
28	718.6	26.5	3871	13	US-10-187-883-347	Sequence 347, App
29	718.6	26.5	3871	13	US-10-194-363-347	Sequence 347, App
30	718.6	26.5	3871	13	US-10-194-460-347	Sequence 347, App
31	718.6	26.5	3871	13	US-10-194-463-347	Sequence 347, App
32	718.6	26.5	3871	13	US-10-194-484-347	Sequence 347, App
33	718.6	26.5	3871	13	US-10-195-884-347	Sequence 347, App
34	718.6	26.5	3871	13	US-10-195-896-347	Sequence 347, App
35	718.6	26.5	3871	13	US-10-196-744-347	Sequence 347, App
36	718.6	26.5	3871	13	US-10-196-755-347	Sequence 347, App
37	718.6	26.5	3871	13	US-10-196-757-347	Sequence 347, App
38	718.6	26.5	3871	13	US-10-197-704-347	Sequence 347, App
39	718.6	26.5	3871	13	US-10-197-710-347	Sequence 347, App
40	718.6	26.5	3871	13	US-10-198-758-347	Sequence 347, App
41	718.6	26.5	3871	13	US-10-198-766-347	Sequence 347, App
42	718.6	26.5	3871	13	US-10-199-304-347	Sequence 347, App
43	718.6	26.5	3871	13	US-10-199-309-347	Sequence 347, App
44	718.6	26.5	3871	13	US-10-199-313-347	Sequence 347, App
45	718.6	26.5	3871	13	US-10-199-456-347	Sequence 347, App

ALIGNMENTS

RESULT 1

US-09-774-490-1
; Sequence 1, Application US/09774490
; Patent No. US20010034332A1
; GENERAL INFORMATION:
; APPLICANT: Jin, Shengfang
; TITLE OF INVENTION: RESISTANCE SEQUENCES AND USES THEREOF
; FILE REFERENCE: 07334-138001
; CURRENT APPLICATION NUMBER: US/09/774,490
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: US 60/179,191
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2709
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-774-490-1

Query Match		100.0%	Score 2709;	DB 9;	Length 2709;
Best Local Similarity		100.0%;	Pred. No. 0;		
Matches 2709;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	AATCTTTTATTTATCGATGTTAAAGCTTAGTAATCGATGCCACGTCCAGGGGTGCG	60		
Db	1	AATCTTTTATTTATCGATGTTAAAGCTTAGTAATCGATGCCACGTCCAGGGGTGCG	60		
Qy	61	ACCACGCGTCGGGAGTGGTTAGCTGCTGCTTCCCATGTCCACGCTCTATTT	120		
Db	61	ACCACGCGTCGGGAGTGGTTAGCTGCTGCTTCCCATGTCCACGCTCTATTT	120		
Qy	121	CCAGATGTTTGAACCTTCTTGCCGCCACAAATACAGAAAGAGACTAAAGCAGCAAGG	180		
Db	121	CCAGATGTTTGAACCTTCTTGCCGCCACAAATACAGAAAGAGACTAAAGCAGCAAGG	180		
Qy	181	GACCTACAGCGTCTGCAGATGGGCTGGTAACTAGGATGTCTGTCTTTCTGGGGAGT	240		

QY 2401 GCAAGGCGGACATACCCAGGGAACAGTAAAGAAATGGAAGCACTTACAGAAATAA 2460
Db 2401 GCAAGGCGGACATACCCAGGGAACAGTAAAGAAATGGAAGCACTTACAGAAATAA 2460
QY 2461 GAAAGGTAGAAACAGGAGGACCCAGAAATTTGAGAGGGAACCCAGGAGTGTCTGAGCTGC 2520
Db 2461 GAAAGGTAGAAACAGGAGGACCCAGAAATTTGAGAGGGAACCCAGGAGTGTCTGAGCTGC 2520
QY 2521 ATTACTCTAGAAACCTCAACAGTAGAGAAATTTGCGCTAGACATATACTGGAAGAAACAA 2580
Db 2521 ATTACTCTAGAAACCTCAACAGTAGAGAAATTTGCGCTAGACATATACTGGAAGAAACAA 2580
QY 2581 TGCAATATACATGAACCTTTTTCATGCGATTATGCGATGTTTACAATGCTGGGAATTC 2640
Db 2581 TGCAATATACATGAACCTTTTTCATGCGATTATGCGATGTTTACAATGCTGGGAATTC 2640
QY 2641 AGCTGAGTTCACCAATATATAATTAATTCATGATGATCTTCTTAATAGGCTTTTTT 2700
Db 2641 AGCTGAGTTCACCAATATATAATTAATTCATGATGATCTTCTTAATAGGCTTTTTT 2700
QY 2701 CCTAATACC 2709
Db 2701 CCTAATACC 2709

RESULT 2
US-10-247-671-83
; Sequence 83, Application US/10247671
; Publication No. US20030194721A1
; GENERAL INFORMATION:
; APPLICANT: Mikita, Thomas
; APPLICANT: Shiffman, Dov
; APPLICANT: Porter, Gordon, J.
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED FOAM CELLS
; FILE REFERENCE: PA-0050 US
; CURRENT APPLICATION NUMBER: US/10/247,671
; CURRENT FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: 60/323,784
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: PERL Program
; SEQ ID NO 83
; LENGTH: 2848
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030194721A1 1930967CB1
US-10-247-671-83

Query Match 92.9%; Score 2517; DB 15; Length 2848;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2517; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 193 CTGAGCATGGCTGGTTAACTAGGATGCTGCTCTTTCTGGGGAGTATTACTTACAGC 252
Db 9 CTGAGCATGGCTGGTTAACTAGGATGCTGCTCTTTCTGGGGAGTATTACTTACAGC 68
QY 253 AAGAGCAAACTATCAGAAATGGAGAAACAAATGCGCAGGCTGAAATTTCTCTCAAGA 312
Db 69 AAGAGCAAACTATCAGAAATGGAGAAACAAATGCGCAGGCTGAAATTTCTCTCAAGA 128
QY 313 AATGTTGGAATCCAAACAAATGATCATCTTCAATGGCTTGGCCCAAGCTCCAGTTATCA 372
Db 129 AATGTTGGAATCCAAACAAATGATCATCTTCAATGGCTTGGCCCAAGCTCCAGTTATCA 188
QY 373 TACCTTCCTTTTGGATGAGGAACGAGTAGGCTGTATGTTGGAGCAAGGATCACATATT 432
Db 189 TACCTTCCTTTTGGATGAGGAACGAGTAGGCTGTATGTTGGAGCAAGGATCACATATT 248
QY 433 TTCATTGCACTGGTTAATATCAAGGATTTTCAAAAGATTTGTGTGCGCCAGTATCTTACAC 492

Db 249 TTCAATTCGACCTGGTTAATATCAAGGATTTTCAAAAGATTTGTGCGCAGTATCTTACAC 308
QY 493 CAGAAGAGATGAATCAAGTGGCTGGAAGAGCATCTCTGAAAGAAATGTCTTAATTTCA 552
Db 309 CAGAAGAGATGAATCAAGTGGCTGGAAGAGCATCTCTGAAAGAAATGTCTTAATTTCA 368
QY 553 CAAGGTACTTTAAGGCATATAATCAGACTCATCTGTACGCTGTGGAAACGGGGCTTTTCA 612
Db 369 CAAGGTACTTTAAGGCATATAATCAGACTCATCTGTACGCTGTGGAAACGGGGCTTTTCA 428
QY 613 TCCAAATTTGACCTCAATGAAATTCGACATCATCTGAGGACAAATATTTTAAAGCTGGA 672
Db 429 TCCAAATTTGACCTCAATGAAATTCGACATCATCTGAGGACAAATATTTTAAAGCTGGA 488
QY 673 GAATCAATTTTGAAGAAACGGCGCTGGGAAGAGTCCATATGACCTTAAAGCTGACAGC 732
Db 489 GAATCAATTTTGAAGAAACGGCGCTGGGAAGAGTCCATATGACCTTAAAGCTGACAGC 548
QY 733 ATCCCTTTTAAATAGATGGAGAAATTAATCTGGAACCTGAGCTGATTTTATGGGGGAGA 792
Db 549 ATCCCTTTTAAATAGATGGAGAAATTAATCTGGAACCTGAGCTGATTTTATGGGGGAGA 608
QY 793 CTTTGCTATCTTCCGAACTCTTGGGCAACCAACCAATCAGGACAGAGCAGCATGATTC 852
Db 609 CTTTGCTATCTTCCGAACTCTTGGGCAACCAACCAATCAGGACAGAGCAGCATGATTC 668
QY 853 CAGGTGCTCAATGATCCAAAGTTCAATAGTCCCACTCATCTCAGAGAGTGACATCTC 912
Db 669 CAGGTGCTCAATGATCCAAAGTTCAATAGTCCCACTCATCTCAGAGAGTGACATCTC 728
QY 913 TGAAGATGACAAAGTATACCTTTTCTCGTGAAATGCAATAGATGAGGAGACATCTCTG 972
Db 729 TGAAGATGACAAAGTATACCTTTTCTCGTGAAATGCAATAGATGAGGAGACATCTCTG 788
QY 973 AAAAGCTACTCAGCTAGAAATAGTGCAGATATGCAAGAAATGATTTGGAGGGGACAGAAG 1032
Db 789 AAAAGCTACTCAGCTAGAAATAGTGCAGATATGCAAGAAATGATTTGGAGGGGACAGAAG 848
QY 1033 TCTGGTGAATTAATGACAAACATTTCTCAAAGCTGCTGATTTGCTCAGTCCAGGCTCC 1092
Db 849 TCTGGTGAATTAATGACAAACATTTCTCAAAGCTGCTGATTTGCTCAGTCCAGGCTCC 908
QY 1093 AAATGGCATGACATCAATTTTGAATGAACTGAGGATGATTTCTTAATGAACTTTAAAGA 1152
Db 909 AAATGGCATGACATCAATTTTGAATGAACTGAGGATGATTTCTTAATGAACTTTAAAGA 968
QY 1153 TCCTAAATCCAGTTGTATATGGAGTGTACGCTTCCAGTAAACATTTTCAAGGGATC 1212
Db 969 TCCTAAATCCAGTTGTATATGGAGTGTACGCTTCCAGTAAACATTTTCAAGGGATC 1028
QY 1213 AGCGTGTGTATGTATAGCATGAGTGTGAGAGGGTGTTCCTTGTCTCATATGCCCA 1272
Db 1029 AGCGTGTGTATGTATAGCATGAGTGTGAGAGGGTGTTCCTTGTCTCATATGCCCA 1088
QY 1273 CAGGGATGACCCAACTATCAATGGTGCCTTATCAAGGAAGTCCCTATCCAGGSC 1332
Db 1089 CAGGGATGACCCAACTATCAATGGTGCCTTATCAAGGAAGTCCCTATCCAGGSC 1148
QY 1333 AGGAATCTTCCAGCAAAACATTTGGTGTTCACCTCAAAAGGACCTTCTCTGATCA 1392
Db 1149 AGGAATCTTCCAGCAAAACATTTGGTGTTCACCTCAAAAGGACCTTCTCTGATCA 1208
QY 1393 TGTATAACCTTTGGAAGAGTCAATCCAGCCATGTAATTCAGTGTCTTCTATGAACAA 1452
Db 1209 TGTATAACCTTTGGAAGAGTCAATCCAGCCATGTAATTCAGTGTCTTCTATGAACAA 1268
QY 1453 TCGCCCAATAGTATCAAAACGGATGTAATTTCAATTTACAAATTTGCTAGACCG 1512
Db 1269 TCGCCCAATAGTATCAAAACGGATGTAATTTCAATTTACAAATTTGCTAGACCG 1328
QY 1513 AGTGAATGCAAGATGGACAGTATGTTTATCGGAACAGATGTTGGGACCGT 1572

Db 1689 AAGAAATGGAGAGCCCTGACTGCTTACAGACTTACACCATGATATCAACCTGGCCA 1748
Qy 1933 CAGCCCTGAAGAGAGATCATCTATGCTGAGAGATAGTAGCACAATTTTGGAAATGCAG 1992
Db 1749 CAGCCCTGAAGAGAGATCATCTATGCTGAGAGATAGTAGCACAATTTTGGAAATGCAG 1808
Qy 1993 TCCGAAGTCCGAGAGAGCGTGGTCTATTGGCAATTCAGAGCGGAAATGAAGAGCGAAA 2052
Db 1809 TCCGAAGTCCGAGAGAGCGTGGTCTATTGGCAATTCAGAGCGGAAATGAAGAGCGAAA 1868
Qy 2053 AGAAGAGATCAGAGTGGATGATCATATCATCAGACAGATCAAGGCGCTTCTGTACGTAG 2112
Db 1869 AGAAGAGATCAGAGTGGATGATCATATCATCAGACAGATCAAGGCGCTTCTGTACGTAG 1928
Qy 2113 TCTACAAAGAGAGATTCAGGCAATTCAGGCTGCGGATGCGGATGCGGATGCGGATGCGGAT 2172
Db 1929 TCTACAAAGAGAGATTCAGGCAATTCAGGCTGCGGATGCGGATGCGGATGCGGATGCGGAT 1988
Qy 2173 AACTCTTTCTTAAGGTAAACCTGGAAGTCTTACAGACAGAGCAATTTTGGAGAACTTCTTCA 2232
Db 1989 AACTCTTTCTTAAGGTAAACCTGGAAGTCTTACAGACAGAGCAATTTTGGAGAACTTCTTCA 2048
Qy 2233 TAAAGATGATGATGAGATGGCTCTTAAGACCAAGAAATGTCATAGCATGACACCTAG 2292
Db 2049 TAAAGATGATGATGAGATGGCTCTTAAGACCAAGAAATGTCATAGCATGACACCTAG 2108
Qy 2293 CCAGAGGCTCTGCTACAGAGACTTTCATGAGCTCATCAACCCCAATCTCAACACGAT 2352
Db 2109 CCAGAGGCTCTGCTACAGAGACTTTCATGAGCTCATCAACCCCAATCTCAACACGAT 2168
Qy 2353 GATGAGTCTGTGAACAGATTTGGAAGAGGACCGAAACAACTGCGCAAGCCAGG 2412
Db 2169 GATGAGTCTGTGAACAGATTTGGAAGAGGACCGAAACAACTGCGCAAGCCAGG 2228
Qy 2413 ACATACCCAGGAGACAGTAAACAAATGGAAGCACTTCAAGAAATTAAGAAAGTAGAAA 2472
Db 2229 ACATACCCAGGAGACAGTAAACAAATGGAAGCACTTCAAGAAATTAAGAAAGTAGAAA 2288
Qy 2473 CAGGAGGACCCAGAAATTTAGAGGCGACCCAGGAGTGTCTGAGTGCATTAACCTCTAGA 2532
Db 2289 CAGGAGGACCCAGAAATTTAGAGGCGACCCAGGAGTGTCTGAGTGCATTAACCTCTAGA 2348
Qy 2533 AACCTCAACAGTAGTAACCTGCTAGACATTAAGTGAAGAAACAAATGCAATATACAT 2592
Db 2349 AACCTCAACAGTAGTAACCTGCTAGACATTAAGTGAAGAAACAAATGCAATATACAT 2408
Qy 2593 GAACCTTTTTCATGCAATTAATGATGATGTTTACATGTTGGAATTCAGCTGAGTTCCA 2652
Db 2409 GAACCTTTTTCATGCAATTAATGATGTTTACATGTTGGAATTCAGCTGAGTTCCA 2468
Qy 2653 CCAATTAATAATTAATCAATGATTAATTTCTTAATAGGCTTTTTC 2702
Db 2469 CCAATTAATAATTAATCAATGATTAATTTCTTAATAGGCTTTTTC 2518

RESULT 5

US-10-067-632-53

; Sequence 53, Application US/10067632

; Publication No. US20030166949A1

; GENERAL INFORMATION:

; APPLICANT: Goodman, Corey S.

; Kolodkin, Alex L.

; Matthes, David

; Bentley, David R.

; O'Connor, Timothy

; TITLE OF INVENTION: The Semaphorin Gene Family

; NUMBER OF SEQUENCES: 100

; CORRESPONDENCE ADDRESS:

; ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP

; STREET: 268 Bush Street, Suite 3200

; CITY: San Francisco

; STATE: CA

; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/067,632
; FILING DATE: 04-Feb-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/060,610
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/835,268
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B94-002-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2601 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 16..2331
; SEQUENCE DESCRIPTION: SEQ ID NO: 53:
US-10-067-632-53

Query Match

Best Local Similarity 92.6%; Score 2508.4; DB 15; Length 2601;
Matches 2509; Conservative 0; Pred. No. 0;
Mismatch 1; Indels 0; Gaps 0;

Qy 193 CTGAGCATGGCTGGTAACTAGGATGCTCTCTTTCTGGGAGTATTTACTTACAGC 252
Db 9 CTGAGCATGGCTGGTAACTAGGATGCTCTCTTTCTGGGAGTATTTACTTACAGC 68
Qy 253 AAGAGCAAACTATCAGATGGGAGAACATATGCGCAAGCTGAAATTTCTTACAAAGA 312
Db 69 AAGAGCAAACTATCAGATGGGAGAACATATGCGCAAGCTGAAATTTCTTACAAAGA 128
Qy 313 AATGTTGGAATCCAAATGTGATCACTTTCAATGGCTTGGCCACAGCTCCAGTTATCA 372
Db 129 AATGTTGGAATCCAAATGTGATCACTTTCAATGGCTTGGCCACAGCTCCAGTTATCA 188
Qy 373 TACCTTCCCTTTGGATGAGGAGGAGTAGGCTGTATGTTGGAGCAAGATCACATATT 432
Db 189 TACCTTCCCTTTGGATGAGGAGGAGTAGGCTGTATGTTGGAGCAAGATCACATATT 248
Qy 433 TTCAATTCGACCTGGTTAATATCAAGGATTTTCAAAAGATTTGTGTGGCCAGTATCTTACAC 492
Db 249 TTCAATTCGACCTGGTTAATATCAAGGATTTTCAAAAGATTTGTGTGGCCAGTATCTTACAC 308
Qy 493 CAGAAGAGATGAATGCAAGTGGCTGGAAAAGACATCTCTGAAAGAAATGTGTAATTTCAAT 552
Db 309 CAGAAGAGATGAATGCAAGTGGCTGGAAAAGACATCTCTGAAAGAAATGTGTAATTTCAAT 368
Qy 553 CAAGGTACTTAAGGCAATTAATCAGATCACTTGTACGCTGTGGAAACGGGGCTTTTCA 612
Db 369 CAAGGTACTTAAGGCAATTAATCAGATCACTTGTACGCTGTGGAAACGGGGCTTTTCA 428
Qy 613 TCAATTTGCACTCAATTTGAAATTTGGACATCATCTGAGGCAATTTTAAAGCTGA 672
Db 429 TCAATTTGCACTCAATTTGAAATTTGGACATCATCTGAGGCAATTTTAAAGCTGA 488

QY 673 GAACCTCACATTTTGAACCGCCGCTGGAGAGTCCATATGACCCCTAAGCTCTGACAGC 732
 Db 489 GAACTCACATTTTGAACCGCCGCTGGAGAGTCCATATGACCCCTAAGCTCTGACAGC 548
 QY 733 ATCCCTTTTATAGATGGAGATATATCTCTGGAATGAGCTGATTTTATGGGCGGAGA 792
 Db 549 ATCCCTTTTATAGATGGAGATATATCTCTGGAATGAGCTGATTTTATGGGCGGAGA 608
 QY 793 CTTTCTATCTTCCGAATCTCTGGGACCAACCACTCCAGACAGAGCAGCATGATTC 852
 Db 609 CTTTCTATCTTCCGAATCTCTGGGACCAACCACTCCAGACAGAGCAGCATGATTC 668
 QY 853 CAGGTGGCTCAATGATCCAAAGTTCAATAGTGGCCCACTCTCATCTCAGAGAGTGAATCC 912
 Db 669 CAGGTGGCTCAATGATCCAAAGTTCAATAGTGGCCCACTCTCATCTCAGAGAGTGAATCC 728
 QY 913 TGAAGATGACAAAGTATATCTTTCTTCCGTAAGATGCAATAGATGGAGAACACTCTGG 972
 Db 729 TGAAGATGACAAAGTATATCTTTCTTCCGTAAGATGCAATAGATGGAGAACACTCTGG 788
 QY 973 AAAAGCTACTCAGCTAGATAGTCAATGATGCAAGATGATCTTGGAGGCGACAGAG 1032
 Db 789 AAAAGCTACTCAGCTAGATAGTCAATGATGCAAGATGATCTTGGAGGCGACAGAG 848
 QY 1033 TCTGGTGAATTAATGGAACAACTCTCCTCAAGCTCGCTGATTTGCTCAGTGCAGAGTCC 1092
 Db 849 TCTGGTGAATTAATGGAACAACTCTCCTCAAGCTCGCTGATTTGCTCAGTGCAGAGTCC 908
 QY 1093 AAATGGCATGACACTCAATTTGATGAACTGCAAGGATGATTCCTAAATGAACTTTAAAGA 1152
 Db 909 AAATGGCATGACACTCAATTTGATGAACTGCAAGGATGATTCCTAAATGAACTTTAAAGA 968
 QY 1153 TCCTAAATTAATGGAACAACTCTCCTCAAGCTCGCTGATTTGCTCAGTGCAGAGTCC 1212
 Db 969 TCCTAAATTAATGGAACAACTCTCCTCAAGCTCGCTGATTTGCTCAGTGCAGAGTCC 1028
 QY 1213 AGCCGTGTGATGATAGTATGATGATGAGAGGATGATTCCTGATGATGATGATGATG 1272
 Db 1029 AGCCGTGTGATGATAGTATGATGATGAGAGGATGATTCCTGATGATGATGATGATG 1088
 QY 1273 CAGGATGAGCCCAACTATCAATGAGTGTGATGATGAGAGGATGATTCCTGATGATGATG 1332
 Db 1089 CAGGATGAGCCCAACTATCAATGAGTGTGATGATGAGAGGATGATTCCTGATGATGATG 1148
 QY 1333 AGGAACCTGTCCAGCAAAACATTTGGTGTGATGATGAGAGGATGATTCCTGATGATGATG 1392
 Db 1149 AGGAACCTGTCCAGCAAAACATTTGGTGTGATGATGAGAGGATGATTCCTGATGATGATG 1208
 QY 1393 TGTATTAACCTTTGCAAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATG 1452
 Db 1209 TGTATTAACCTTTGCAAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATG 1268
 QY 1453 TCGCCCAATAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1512
 Db 1269 TCGCCCAATAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1328
 QY 1513 AGTGGATGCAAGATGAGCAGTATGATGATGATGATGATGATGATGATGATGATGATGATG 1572
 Db 1329 AGTGGATGCAAGATGAGCAGTATGATGATGATGATGATGATGATGATGATGATGATGATG 1388
 QY 1573 TCTTAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1632
 Db 1389 TCTTAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1448
 QY 1633 AGAATGCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1692
 Db 1449 AGAATGCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1508
 QY 1693 GCAACCACTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1752
 Db 1509 GCAACCACTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1568
 QY 1753 TATTTACGGAGGAGCGGTGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1812

Db 1569 TATTTACGGAGGAGCGGTGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1628
 QY 1813 TGGTTCTGATGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1872
 Db 1629 TGGTTCTGATGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1688
 QY 1873 AAGAAATGAGAGCCCACTGACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1932
 Db 1689 AAGAAATGAGAGCCCACTGACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1748
 QY 1933 CAGCCCTGAGAGAGAAATCATCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1992
 Db 1749 CAGCCCTGAGAGAGAAATCATCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1808
 QY 1993 TCCGAAGTCCGAGAGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2052
 Db 1809 TCCGAAGTCCGAGAGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1868
 QY 2053 AGAAGAGATCAGAGTGGAGTATCATATCATCAGAGAGATCAGAGGCTTCTGCTGCTGCTGCTG 2112
 Db 1869 AGAAGAGATCAGAGTGGAGTATCATATCATCAGAGAGATCAGAGGCTTCTGCTGCTGCTGCTG 1928
 QY 2113 TCTACACAGAGAGATCAGAGTGGAGTATCATATCATCAGAGAGATCAGAGGCTTCTGCTGCTGCTGCTG 2172
 Db 1929 TCTACACAGAGAGATCAGAGTGGAGTATCATATCATCAGAGAGATCAGAGGCTTCTGCTGCTGCTGCTG 1988
 QY 2173 AACTCTTCTTAAAGGTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2232
 Db 1989 AACTCTTCTTAAAGGTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2048
 QY 2233 TAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2292
 Db 2049 TAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2108
 QY 2293 CCAGAGAGTCTGGTACAGAGACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2352
 Db 2109 CCAGAGAGTCTGGTACAGAGACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2168
 QY 2353 GGATGAGTCTGTGAAAGTGTGGAAAGGAGCCGAAAGAGAGTGTGGGAAAGGAGGAGG 2412
 Db 2169 GGATGAGTCTGTGAAAGTGTGGAAAGGAGCCGAAAGAGAGTGTGGGAAAGGAGGAGG 2228
 QY 2413 ACATACCCCGAGGAGAGTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2472
 Db 2229 ACATACCCCGAGGAGAGTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2288
 QY 2473 CAGGAGGAGCCCAAGATTTGAGAGGAGCCAGAGAGTGTGAGCTGCTGCTGCTGCTGCTGCTG 2532
 Db 2289 CAGGAGGAGCCCAAGATTTGAGAGGAGCCAGAGAGTGTGAGCTGCTGCTGCTGCTGCTGCTG 2348
 QY 2533 AACCTCAACCAAGTAGAGAACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2592
 Db 2349 AACCTCAACCAAGTAGAGAACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2408
 QY 2593 GAACTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2652
 Db 2409 GAACTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2468
 QY 2653 CCAATTATAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2702
 Db 2469 CCAATTATAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2518

RESULT 6

US-10-404-438-2
 ; Sequence 2, Application US/1040438
 ; Publication No. US20030232411A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Onco Pharmaceutical Co., Ltd.
 ; TITLE OF INVENTION: NOVEL POLYPEPTIDE, cDNA ENCODING THE SAME, AND USE THEREOF
 ; FILE REFERENCE: Q59878
 ; CURRENT APPLICATION NUMBER: US/10/404,438

; CURRENT FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: US/09/582,419A
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: PCT/JP98/05952
; PRIOR FILING DATE: 1998-12-25
; PRIOR APPLICATION NUMBER: P. Hei. 9-358811
; PRIOR FILING DATE: 1997-12-26
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2
; LENGTH: 2331
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-404-438-2

Query Match 26.5%; Score 718.6; DB 16; Length 2331;
Best Local Similarity 61.9%; Pred. No. 5e-206;
Matches 1233; Conservative 0; Mismatches 739; Indels 21; Gaps 5;

QY 269 AATGGGAAGACAAATGTCGACAGGCTGAAATATCTTACAAAGAAATGTTGAAATCCCAAC 328
DB 109 ACTTTGAACAAATATTCAGAGCTCAAGCTAAACCTACAAAGACTTGCCTTCAAAAT 168

QY 329 AATGTGATCACTTCAATGGCTTGGCCAAACAGCTCCAGTTATCATACACCTTCCCTTTGGAT 388
DB 169 AGCTGATTCCTTTTGGGTTTCATCAGAGGACTGGATTTCAAACCTTCTCTTAGAT 228

QY 389 GAGGACGAGTAGGCTGTATGTTGGAGCAAGGATTCATATTTTCAATGACCTGGT 448
DB 229 GAGGAAGAGGAGGCTGCTTCTTGGAGCCAAAGACCACATCTTCTACTCAGTCTGGT 288

QY 449 AA---TATCAAGGATTTTCAAAGATGTCGCCAGATCTTACACCAAGAGAGATCAA 505
DB 289 GACTTAACAAATTTTAAGAGATTTATGGCTGCTGCAAGAGCGGTGGAATTA 348

QY 506 TGCAGTGGGCTGGAAGACATCTCGAAGAAATGTCTAAATTCATCAAGTACTTAAG 565
DB 349 TGTAAATAGCTGGGAAGATGCCAATACAGAAATGTGCAAAATTTTCATCAGAGTCTTCAG 408

QY 566 GCATATAATCAGACTCACTGTACGCTGTGAACGGGGCTTTTCATCCATTTGCACC 625
DB 409 CCTATACAAACTCACAATATGTGTGGAACTGGAGCATTTTCATCCAAATATGTGG 468

QY 626 TACATTTGAATTTGGACATCATCTCTGAGGACAAATATTTTAAGCTGGAGAACTCAATTTT 685
DB 469 TATATTGATCTTGGAGCTTACAAGGAGGATATTAATTCAACTAGACACACGTAATTG 528

QY 686 GAAAAGCGCGTGGGAGAGTCCATATGACCTTAAGCTGTGACAGCATCCCTTTTAATA 745
DB 529 GAGTCTGGGAGACTGAAAATGTCTTTTCGATCCTCAGCAGCCCTTTTGTCTCAGTAATGACA 588

QY 746 GATGGAGAAATTAATCTCTGGAATCTGAGTGAATTTATGGGCGAGACTTTTGTCTATCTTC 805
DB 589 GATGAGTACCTCTACTCTGGAACAGCTTCTGATTTCTTGGCAAGATACCTGATCTACT 648

QY 806 CGAATCTTTGGGC-----ACCACCAACCAATCAGGACAGCAGCAGCATGATTCACAG 856
DB 649 CGATCCCTTGGGCTTACTCATGACCACCACTACATCAGAACTGACATTTTCAGAGCACTAC 708

QY 857 TGGCTCAATGATCCAAAGTTCAATTAGTCCCACTCATCTCAGAGAGTGAATCCCTGAA 916
DB 709 TGGCTCAATGAGCAAAATTTATGGAATCTTTTACACAGACCATCAATCCAGAT 768

QY 917 GATGACAAAGTATACCTTTTCTTCGTTGAAAATGCAATPAGATGGAGAACACTCTGGAAAA 976
DB 769 GATGATAAAATATAATTTCTTCTTCTGTAATCATCTCAAGAGGCGAGTACCTCCGATAAA 828

QY 977 GCTACTCAGCTAGAAATAGTTCAGATATGCAAGATGACTTTGAGGGCAAGAGTCTG 1036
DB 829 ACCATCTTCTCGAGTTGGAAGAGTTTGTAAAGATGATGTAGGAGGACCAACGAGCGCTG 888

QY 1037 GTGAATAAATGACAACTTCTCTCAAGCTGTCTGATTTGCTCAGTCCAGGTCCTCAAT 1096

DB 889 ATAAACAAGTGGACGACTTTTCTTTAAGGCCACGACTGATTTGCTCAATTCCTGGAAGTAT 948
QY 1097 GGCATTGACACTCACTTTTGTATGACTGACGATGATATTCCTAATGAATTTAAAGTCCCT 1156
DB 949 GGGCAGATCTTACTTTGATGAGCTTCAAGATATTTATTTACTCCCAACAGAGATGAA 1008
QY 1157 AAAAATCCAGTTGTATATGGAGTGTTTACGACTTCCAGTAACATTTTCAAGGGATCAGCC 1216
DB 1009 AGAAATCCTGTAGTATATGGAGTCTTTACTACAACACGACTCCATCTTTCAAAGGCTCTGCT 1068
QY 1217 GTGTGTATGTATGATGATGATGATGAGAGGGTGTCTTGTGTCATATGCCACAGG 1276
DB 1069 GTTTGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1128
QY 1277 GATGGACCCAACTATCAATGGGTGCTTTATCAAGAAAGAGTCCCTATCCACGCGCCAGGA 1336
DB 1129 GAAAGTGCAGACCACTGCTGGGTGCTAGTATGATGGAGAAATTCCTTATCCACGCGCTGGT 1188
QY 1337 ACTTGTCCCAAGCAAAATTTG---GTGGTTTGTACTCTACAAGGACCTTCTCTGATGAT 1393
DB 1189 ACATGTCCAAAGCAAAACCTATGACCCCACTGATTAAGTCCACCCGAGATTTTCCAGATGAT 1248
QY 1394 GTTATAACCTTTGCAAGAAGTCCATCCAGCCATGTACAATCCAGTGTTCCTATCAACAAT 1453
DB 1249 GTCATCAGTTTCATAAAGCGCACTCTGTGATGTATGATGATGATGATGATGATGATGATGAT 1308
QY 1454 CGCCCAATAGTGTATCAAAACGGATGTAATTAATTAACAATAATGTCGTAGACCGA 1513
DB 1309 GGACCAACGTTCAAGAGATCAATGTGGATTTACAGACTGACACAGATAGTGGTGGATCAT 1368
QY 1514 GTGATCCAGAAGATGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1573
DB 1369 GTCATTCGAGAGATGCGCAGTACGATGATGATGATGATGATGATGATGATGATGATGATGAT 1428
QY 1574 CTTAAAGTGTCTCAATTCCTTAAGGAGACTTGGTATGATGATTTAGAGAGGTTCTGCTGGA 1633
DB 1429 CTCAAAGTGTGACATTTCAAAGGAAAAGTGG---AATATGGAAGAGGTTAGTGTGAG 1485
QY 1634 GAAATGACAGCTTTTCCGGAACCGACTGTCTATTTACAGATGAGCTTTTCCATTAAGCAG 1693
DB 1486 GAGTTGAGATATTCAGACACTCATCAATCATCTTGAACATGGAATTTGTCTCTGAAGCAG 1545
QY 1694 CAACAACTATATTTGTTTCAAGGCTGGGTTTCCGAGCTCCCTTTTACACCGGTGTGAT 1753
DB 1546 CAACATTTGATGTTTCCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1605
QY 1754 ATTTACGGGAAAGCTGT 1813
DB 1606 ACTTATGGGAAAGCTTTGCGCAGACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1665
QY 1814 GGTTCGTCATGTTCTGCTATTTTCCACTGCAAGAGAGCGCAACAGACGACAGATATA 1873
DB 1666 GGAATGCTATGCTCTCGATATGCTCTCTCTTCTTAAAGAGAGAGCTAGACCCAGATGTA 1725
QY 1874 AGAAATGGAGACCCACTGACTACTGTTCAGACTTACCACTGATTAATCAACCATGCCAC 1933
DB 1726 AAATATGGGACCCCAATCACCCAGTGTGGGACATCGAAGACAGCATTAAGTATG---AA 1782
QY 1934 AGCCCTGGAAGAGAGATCATCTATGTTGTAGAGATAGTAGACATTTTGGNATCGAGT 1993
DB 1783 ACTGCTGATGAAAAGGTGATTTTGGCATTTGAATTTAACTCAACCTTTCTGGAATGTATA 1842
QY 1994 CCGAAGTCCGAGAGAGCGGTGTTCTATTGGCAATTCAGAGGCGAAATGAAGAGCGAAAA 2053
DB 1843 CCTTAATCCCAACGAACACTATTAATGGTATATCCAGAGGTTCAGGGGATGAGCATCGA 1902
QY 2054 GAAGAGATCAGAGTGTGATGATCATATCATCAGAGACAGATCAAGCCCTTCTGTACCTAGT 2113
DB 1903 GAGGAGTTGAAGCCCGCATGAAAGATCATCAAAACCGAATATGCGGTACTGATTCGAAAGT 1962
QY 2114 CTACAAACAGAGGATTTGAGCAATTAACCTCTGCGATGCGGTGGAACATGGGTTTCAACAA 2173
DB 1963 TTGCAAGAGAGGATTTCTGGGATGATTAATCTGCAAGGCCAGGACGACACTTTTATCCAC 2022

OY 2174 ACTCTTCTTAAGTAACCTGGAAGTCATTGACACAGAGCATTGGAGAAGACTTCTTCAT 2233
Db 2023 ACCATAGTGAAGCTGACTTGTGAATGTCTTGAATGAACATGAGATAATACCCAGAGG 2082
OY 2234 AAGATGATGATG 2246
Db 2083 GCAGAGCATGAGG 2095

RESULT 7

US-09-946-374-309
; Sequence 309, Application US/09946374
; Publication No. US20030073129A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Pacini, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1
; CURRENT APPLICATION NUMBER: US/09/946,374
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098836
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/098596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/098598
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/098602
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/098642
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099741
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099754
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099763
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099792
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099808
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099812
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099815
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099816
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/100385
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100388
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100390
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100584
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100627
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100661
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100662
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100664
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100683
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100684
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100710
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100711
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100848
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100849
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100919
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100930
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/101014
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101068
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101071
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101279
; PRIOR FILING DATE: 1998-09-22
; PRIOR APPLICATION NUMBER: 60/101471
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101472
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101474
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101475
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101476
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101477
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101479
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101738
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101741
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101743
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101915
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101916
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/102207

[illegible]

QY	1394	GTATATACTTTGGAAGAAGTCATCCAGCCAGTGAACAATCCAGTGTTCCTATGAAACAAT	1453
Db	1355	GTCAATCAGTTTCAATAAAGCGGCACCTGTGTGATGTATAAGTTCGGTATACCACAGTTGCGAGGA	1414
QY	1454	CGCCCAATAGTAGTCAAAACGGAGTGAATAATTCAATTTACAAATTTGTCGTAGACCGGA	1513
Db	1415	GGACCAACGTTCAAGAGATCAATGTGGATTACAGACTGACACAGATAGTGGTGCATCAT	1474
QY	1514	GTGGATCGAGAAGATGGACAGTATGATGTATGTTTATCGGAACAGATGTTGGGACCGGTT	1573
Db	1475	GTCAATTGCGAAGATGCGCCAGTACGATGTAATGTTCTTTGGAAACAGACANTGGAACCTGTC	1534
QY	1574	CTTTAAAGTAGTTTCAATTTCTTAAGGAGACTTGGTATGATTTTGAAGAAGAGTCTCTGCTGAA	1633
Db	1535	CTCAAGTGTTCAGCATTTCAAGGAAAAGTGG---AATATCGAAGAGGTAGTCTCTGGAG	1591
QY	1634	GAAATGACAGTTTTTCGGGAACCGAGCTGATTTTTCAGCAATGGAGCTTTTCCACTAAGCAG	1693
Db	1592	GAGTTGCGAGATATTCAAAGCACTCATCAATCATCTTGAACATGGAAATGCTCTCTGAAGCAG	1651
QY	1694	CAACAACATATATATTGGTTCAACGGCTGGGGTTGCCACGCTCCCTTTACCGCGGTGTGAT	1753
Db	1652	CAACAATTTGTACATTGGTTCCGAGATGGATAGTTTCACTCTCCCTCGACAGATGGCAC	1711
QY	1754	ATTTACGGGAAGCGTGTGTGATGTGTGCTGCCCGAGAGCCCTTACTGTGCTTGGGAT	1813
Db	1712	ACTTATGCGGAAGCTTCGCAGAGCTGTGTGCTTTGCCAGAGACCCCTACTGTGCTCGGGAT	1771
QY	1814	GGTTCTGCATCTCTCCGCTATTTTCCCACTGCAAGAGAGCGCACAGAGCACAAGATATA	1873
Db	1772	GGAAATGCATGCTCTCGATATGCTCTTACTTTAAAGGAGAGCTTAGAGCCCAAGATGTA	1831
QY	1874	AGAAATGGAGACCCTGACTCACTGTTCAGACTTACACCATGATPAATCACCATGGCCAC	1933
Db	1832	AAATATGCGGACCCAATCCACGAGTGTGGGACATCGAAGACAGCATTAGTCAATG---AA	1888
QY	1934	AGCCCTGAAGAGAGAACTCATCTATGTGTAGAGAAATAGTAGACACATTTTTCGAAATGCAGT	1993
Db	1899	ACTGCTGATGAAGAGTGATTTTGGCATTTGAATTTTACTCAACCTTCTCGAAATGTATA	1948
QY	1994	CGAAGTCGAGAGAGCGCTGGTCTATTTGGCAATTCAGAGCGGAATTAAGAGCGGAAA	2053
Db	1949	CTTAATCCCAACAAGCAAATAATTAATGGTATATCCAGAGTCAAGGGATGAGCATCGA	2008
QY	2054	GAAAGATTCAGATGGAGTATCATATCNCAGACAGATCAAGGCCCTTCTGCTACGTAGT	2113
Db	2009	GAGGATTTGAAGCCGATGAAGAAATCATCAAAACGGAATATGGGCTACTGATTCGAAGT	2068
QY	2114	CTACAACAGAAGGATTGAGCAATTTACCTTGCCATGGCGTGGAAATGSGGTTTCATCAA	2173
Db	2069	TTGCAGAGAAGAGGATCTGGGATGTATTAATGCAAGGCCAGGAGCACACTTTCATCCAC	2128
QY	2174	ACTCTTCTTAGGTAAACCTCGAAGTCATTCACAGAGCATTTTGGAGAGACTTCTTTCAT	2233
Db	2129	ACCATAGTGAAGCTGACTTTGAAATGTCATTTGGAATGAACAGATGGAAATATCCAGAGG	2188
QY	2234	AAAGATGATGATG 2246	
Db	2189	GCAGAGCATGAGG 2201	

RESULT 8

US-10-015-395A-309
; Sequence 309, Application US10015395A
; Publication No. US20040073015A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman

QY 977 GCTACTCAGCTAGATAGTCTAGATATGCAAGATGACTTTGGAGGGCACAGAAGTCTG 1036
Db 935 ACCATCTCTTCTCGAGTGGAGAGTGTGTAAGAAATGATGTAGGAGCAACGCGAGCTG 994
QY 1037 GTCAATAAATGGACACATCTCCTAAAGCTGCTGCTGATTTGCTGAGTGCAGGTCAGAT 1096
Db 995 ATAAACAAGTGGACAGCTTTCTTAAAGGCGCAGACTGATTTGCTCAATTCCTCGAAGTGTAT 1054
QY 1097 GGCATTGACACTCATTTTATGATGAATGCGAGGATGATTCCTTAATGAATTTTAAAGATCT 1156
Db 1055 GGGCGAGATATCTTACTTGTAGCTTCAAGATATTTTACTCCCAACAGAGATGAA 1114
QY 1157 AAAATCCAGTTGTATGATGAGTGTATGAGCTTCCAGCTTCCAGGATGATGAGCT 1216
Db 1115 AGAATCCCTGTAGTATATGAGTGTCTTACTCAACCCAGCTCCATCTTCAAGGCTCTGCT 1174
QY 1217 GTGTGTATGTATAGCATGATGATGAGAGGCTGCTTCTTGGTCCATATGCCACAGG 1276
Db 1175 GTTGTGTATGATGATGATGATGAGAGGCTGCTTCTTGGTCCATATGCCATAG 1234
QY 1277 GATGGACCAACTATCAATGGGTGCTTATCAAGGAAGAGTCCCTATCCAGGCGCAGGA 1336
Db 1235 GAAAGTGCAGACCATCGTTGGGTGCGATGATGAGGAGATTCCTTATCCAGGCTGCT 1294
QY 1337 ACTGTGCCAGCAACATTTG---GTGGTTTGTACTCTACAAAGACCTTCTCTGATGAT 1393
Db 1295 AGATGCCAGCAACCTATGACCCACTGATTAAGTCCACCGAGATTTTCCAGATGAT 1354
QY 1394 GTTATAACCTTTGCAAGAGTATCATCGACCATGTATCAATCCAGTGTTCCTATGAACAT 1453
Db 1355 GTCATCAGTTTCATAAAGCGGCACTCTGTGATGATAGTCCGTATACCCAGTTCGAGA 1414
QY 1454 CGCCCAATAGTATCAAAAGGATGTAAATATCAATTTACAAATTTGCTGAGACGGA 1513
Db 1415 GGACCAAGCTTCAAGAGATCAATGTGGATTAACAGCTGACACAGATAGTGTGATCAT 1474
QY 1514 GTGGATGCAAGAGATGAGCATGATGATGATGATGATGATGATGATGATGATGATGAT 1573
Db 1475 GTCAATGCAAGATGAGGCGAGTACGATGTAATGTTTCTTGGACAGATTTGGAATGTC 1534
QY 1574 CTTAAAGTATTTCAATTCCTAAGGAGACTTGGTATGATTTAGAAAGAGTTCTGCTGGA 1633
Db 1535 CTCAAAGTTGTGAGCATTTCAAAGGAAAAGTGG---AATATGGAAGAGTGTGCTGGAG 1591
QY 1634 GAAATGACAGTTTTCGGGAACGAGCTGCTATTTCCAGCAATGAGCTTTCACCTAAGCAG 1693
Db 1592 GAGTTGAGATATCAAGCATCTCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 1651
QY 1694 CAACAACTATATATTTGGTTCAACGGCTGGGGTTGCCAGCTCCCTTTACACGGGTGTGAT 1753
Db 1652 CAACAAATGTACATTTGGTTCCCGAGATGATGATGATGATGATGATGATGATGATGATGAT 1711
QY 1754 ATTTACGGGAAGCTGTGAGTGTGCTCGCCCGAGACCTTTACTGTGCTTGGAT 1813
Db 1712 ACTTATGGAAGCTGTGCGAGACTGTTGTCTGCGAGAGACCCCTACTGTGCTGCGAT 1771
QY 1814 GGTCTGCTGATGTTCTGCTGATTTTCCCACTGCAAGAGACGCAACAGAGCAAGATATA 1873
Db 1772 GGAATGATGCTGCTGATATGCTCTTACTTCTAAAGAGAGCTAGACGCAAGATGTA 1831
QY 1874 AGAATGAGAGCCCACTGACTGCTGTTGAGACTTACACCATGATATACCATGGCCAC 1933
Db 1832 AAATATGCGACCAATCACCCAGTGTGGGACATCGAAGACAGCATTAGTATG---AA 1888
QY 1934 AGCCCTGAAGAGAGATATCTATGTTGTAGAGATAGTACACATTTTGGATGAGT 1993
Db 1889 ACTGCTGATGAAGGATGATTTTGGCATGATTAATTAATTAATTAATTAATTAATTAATTA 1948
QY 1994 CCGAAGTCCGAGAGAGGCTGCTTATTTGGCAATTCAGAGGCGAATGAAGAGCGGAAA 2053
Db 1949 CCTAATCCCAACAGCAACTATTAATGATGATATATCCAGAGGTGAGGGGATGACATCGA 2008
QY 2054 GAAGATCAGAGTGGATGATCATCATCAGGACAGATCAAGGCTTCTGCTACGTAGT 2113

Db 2009 GAGAGTTGACCCGATGAAGATCATCAAAACGGAATATGGCTACTGATTCGAAGT 2068
QY 2114 CTACAAACAAGAGGATTCAGCAATTAACCTCTGCCATCGGTGGAAACATGGGTTTCATACAA 2173
Db 2069 TTGAGAAGAAGAGTTCCTGGATGATTAATTAATTAATTAATTAATTAATTAATTAATTA 2128
QY 2174 ACTCTTCTTAGGTAACCTTGGAGTCTATTTGACACAGAGCATTTGGGAAGACTTCTTCAT 2233
Db 2129 ACCATAGGAAGCTGATTTGAATGTCTTGAATGAATGAACAGATGGAATAACCCAGAGG 2188
QY 2234 AAAGATGATGATG 2246
Db 2189 GCAGAGATGAGG 2201

RESULT 9
US-10-206-915-347
; Sequence 347, Application US/10206915
; Publication No. US20040029221A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C513
; CURRENT APPLICATION NUMBER: US/10/206,915
; CURRENT FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 347
; LENGTH: 3871
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-206-915-347

Query Match 26.5%; Score 718.6; DB 13; Length 3871;
Best Local Similarity 61.9%; Pred. No. 7.4e-206;
Matches 1233; Conservative 0; Mismatches 739; Indels 21; Gaps 5;
QY 269 AATGGGAAGAACAAATGTCACAGGCTGAATATCTCAAAAGAAATGTTGGAATCCAAAC 328
Db 215 ACTTTGAAGAAATATATCCAGACTCAAGCTCAAGACTTGTCTGCTTTCAAT 274

QY 329 AATGTGATCACTTTCAATGCTTGGCCAAACAGCTCCAGTTATCATACCTTCTCTTTGGAT 388
Db 275 AGCTGTATTCCTTTTGGTTCATCAGAGAGCTGGATTTTCAAACCTCTCTTAGAT 334
QY 389 GAGAAACGGAGTAGCTGTATGTGGAGCAAGAGATCACAATTTTCAATTCGACCTGTT 448
Db 335 GAGAAAGAGCGAGCTGCTTTGGGAGCAAGAGCAATCTTTCTACTCAGTCTGGTT 394
QY 449 AA---TATCAAGATTTTCAAPAGATTGTGSCCAGTATCTTACACAGAGAGATGAA 505
Db 395 GACTTAACAAAATTTTAAAGATTTTATGGCTGTCTGCAAGAGAGCGGTGAATTA 454
QY 506 TGAAGTGGCTGGAAAGACATCTTGAAGAGATGTCTTAATTTTCAAGAGTACTTAAG 565
Db 455 TGTAAATAGCTGGGAAAGATGCAATACAGAGATGTGCAATTTTCAATCAGAGTACTTCAG 514
QY 566 GCATATAATCAGACTCACTTGTACGCTGTGGAAAGGGGCTTTTCATCCCAATTTGCACC 625
Db 515 CCTATTAACAAAATTTTAAAGATTTTATGGCTGTCTGCAAGAGAGCGGTGAATTA 574
QY 626 TACATTAATTTGAAGATCATCTGAGGACATATTTTAAAGTGGAGATCTCAATTTT 685
Db 575 TATATTTGATCTTGAAGTACAAAGAGAGATATTTATTTCAAACTAGACACACATAATTTG 634
QY 686 GAAAGCGGCGTGGGAGAGTCCATATGACCTTAAGCTGCTGACAGCATCTCTTTTAATA 745
Db 635 GAGTCTGGCAGACTGAAATGTCTTTTCGATCTCAGAGCTTTTGTCTTCAATGACA 694
QY 746 GATGGAGATTTACTCTGGAATCTGAGTGAATTTTATGGGCGAGACTTTTGTCTATCTTC 805
Db 695 GATGAGTACCTTACTCTGGAACAGCTTCTGATTTCTTGGCAAGAGTACTGCAATTTACT 754
QY 806 CGAATCTTGGGC-----ACCACCAACCAATCAGACAGAGACGATGATTTCCAGG 856
Db 755 CGATCCCTTGGGCTACTCATGACCAACCACTACATCAGACTGCAATTTTCAAGAGCTTAC 814
QY 857 TGGCTCAATGATCAAGTCTTACTGAGTCCCTGATCTCAGAGAGTGAACAATCTGAA 916
Db 815 TGGCTCAATGAGCAAAATTTATGGAACTTTCTTCAATACCAAGAGCTTCAATCCAGAT 874
QY 917 GATGACAAAGTATATTTTCTTCCGTGAATGCAATGATGAGAGACATCTTGGAAA 976
Db 875 GATGATTAATATATTTCTTCTTCTGATCATCTCAAGAGGAGTACTCTCGATTA 934
QY 977 GCTACTCACCTAGATAGTCTAGATATCAAGATGATTTTGGAGGCAAGAGTCTG 1036
Db 935 ACCATCTTTCTCGAGTGGAGAGTTTGTAAAGATGATGAGGAGGCAACAGCGAGCTG 994
QY 1037 GTGAATAATGGACACATTTCTCAAGCTCTGATTTGCTCAGTCCAGGTCCTCAAT 1096
Db 995 ATAAACAGTGGAGAGCTTTCTTAAAGCCAGACTGATTTGCTCAATTTCTTGGAGTAT 1054
QY 1097 GGCATTTGACACTCAATTTGATGAACTGAGGATGATTTCTTAATGAACTTTTAAAGATCT 1156
Db 1055 GGGGCGACATCTTACTTTGATGAGCTTCAAGATTTTATTTACTCTCCCAAGAGATGAA 1114
QY 1157 AAAATCCAGTGTATGAGTGTGTTTACGATCTCAGTAACTTTTCAAGGATCAGCC 1216
Db 1115 AGAATCCCTGATATGAGTCTTTTACTTAAACAGCTCATCTTCAAGGCTCTGCT 1174
QY 1217 GTGTGATGATGAGTATGATGAGAGGGTGTCTTGTGTCATATGCCACAGG 1276
Db 1175 GTTGTGTGATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGT 1234
QY 1277 GATGGACCCCAATCAATGGGTGCTTATCAAGAGAGTCCCTTATCCACGCGCAGGA 1336
Db 1235 GAAAGTGCACACCATCTTGGGTGAGTATGATGAGGAGATTTCTTATCCAGGCTTGT 1294
QY 1337 ACTTGTCCAGCAAAACATTTG---GTGGTGTGATCTTCAAGAGACCTTCTCTGATGAT 1393
Db 1295 ACATGTCCAGCAAAACCTATGACCACTGATTAAGTCCACCGAGATTTTCCAGATGAT 1354
QY 1394 GTTATAACCTTTTCAAGAGTATCATCCAGCATGTACAACTCCAGTGTCTTCTATGAACAT 1453

Db 1355 GTATCAGTTTTCATAAAGCGCACTCTGTGATGTATAGTCCGTATACCCAGTTCGAGGA 1414
QY 1454 CCCCCAATAGTATCAAAACGGATGTAAATTTATCAATTTACAAATTTGCTGTAGACCGA 1513
Db 1415 GGACCAACGCTTCAAGAGAAATCAATGTGGATTTACAGATGACACAGATAGTGGTGGATCAT 1474
QY 1514 GTGGATGACAGAGATGAGACAGTATGATTTATGTTTATCGGAAACAGATGTTGGGACCGT 1573
Db 1475 GTCAATTCAGAGATGAGGCGCACTGATGATTTCTTGGAAACAGACATTTGGAATGTC 1534
QY 1574 CTTAAAGTATGTTTCAATTTCTTAAAGAGACTTGGTATGATTTAGNAGAGTCTTCTGGA 1633
Db 1535 CTCAAAGTGTGACATTTCAAGGAAAGTGG---AATATGGAAAGAGGTAGTGTGGAG 1591
QY 1634 GAAATGACAGTTTTTCGGGAAACCGACTGCTATTTTCAGCAATGGAGCTTTCCACTAAGCAG 1693
Db 1592 GAGTTGCAAGATTTCAAGCACTCATCATCTTGAACATGGAATTTGCTCTGAGGAGCAG 1651
QY 1694 CAAACACTATATTTGTTTCAACGCTGGGTTGCCAGCTCCCTTTTACACCGGTGTGAT 1753
Db 1652 CAACAATTTGATTTGTTTCCCGAGATGGATTTAGTTTCACTCTCTTTCACAGATGGCAG 1711
QY 1754 ATTTACGGGAAAGCTGTGCTGAGTGTTCCTCCCGAGACCTTACTCTGTCTTGGGAT 1813
Db 1712 ACTTATGGGAAAGCTTGGCAGACTGTTGCTTCCAGAGACCTTACTGTGCTGGAT 1771
QY 1814 GGTTCGATGTTTCTGCTATTTTCCCACTGCAAGAGAGACGCAAGAGATATA 1873
Db 1772 GGAATGATGCTGCTGATATGCTTCTTCTTCTTAAAGAGAGCTAGACCCCAAGATGA 1831
QY 1874 AGAATGGAGACCCCACTGACTCACTGTTTCAAGCTTACCACTGATATCAATCAGGCTCCAC 1933
Db 1832 AATATGGCGACCAATCACCCAGTGTGGACATCGAAGACAGCACTTACTCATG---AA 1888
QY 1934 AGCCTGAGAGAGAGATCATCTATGTTGTAGAGATAGTAGCACAATTTTGGATGAGT 1993
Db 1889 ACTGCTGATGAAAGGAGTATTTTGGCAATGAAATTTAACTCAACCTTTCTGGAATGTATA 1948
QY 1994 CCGAAGTGGCAGAGAGCGCTGCTTATTTGGCAATTTCCAGAGGGGAAATGAAGAGCGAAA 2053
Db 1949 CCTAATCCCACAGCAACTATTTAAATGTTATATCCAGAGGTCAGGGATGAGATCGA 2008
QY 2054 GAAGAGATCAGAGTGGATGATCATCATCAGGACAGATCAAGGCTTCTGCTAGTAT 2113
Db 2009 GAGGATTTGAAGCCCGATGAAAGAAATCATCAAAACGGAATATGGGCTACTGATTCGAA 2068
QY 2114 CTACAACAGAGGATTCAGGCAATTTAGCTCTGCCATCGGTGGAAACATGGGTTTACACAA 2173
Db 2069 TTGCAGAGAGAGGATTTCTGGATGTTTACTTGCAAGCCCGAGGACACATTTTATCCAC 2128
QY 2174 ACTTCTTTAAGGTAACCTGGAAGTATGACACAGAGATTTGAGAGTCTTCTTCTCAT 2233
Db 2129 ACCATAGTGAAGCTGACTTTTGAATGTCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2188
QY 2234 AAGATGATGATG 2246
Db 2189 GCAGAGATGAGG 2201

RESULT 10

US-10-199-670-347
; Sequence 347, Application US/10199670
; Publication No. US2004003560A1

GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; TITLE OF INVENTION: ACIDS ENCODING THE SAME
 ; FILE REFERENCE: P3430R1C401
 ; CURRENT APPLICATION NUMBER: US/10/199,670
 ; CURRENT FILING DATE: 2002-07-19
 ; PRIOR APPLICATION NUMBER: 10/052586
 ; PRIOR FILING DATE: 2002-01-15
 ; PRIOR APPLICATION NUMBER: 60/059263
 ; PRIOR FILING DATE: 1997-09-18
 ; PRIOR APPLICATION NUMBER: 60/059266
 ; PRIOR FILING DATE: 1997-09-18
 ; PRIOR APPLICATION NUMBER: 60/062250
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/063120
 ; PRIOR FILING DATE: 1997-10-24
 ; PRIOR APPLICATION NUMBER: 60/063121
 ; PRIOR FILING DATE: 1997-10-24
 ; PRIOR APPLICATION NUMBER: 60/063486
 ; PRIOR FILING DATE: 1997-10-21
 ; PRIOR APPLICATION NUMBER: 60/063540
 ; PRIOR FILING DATE: 1997-10-28
 ; PRIOR APPLICATION NUMBER: 60/063541
 ; PRIOR FILING DATE: 1997-10-28
 ; PRIOR APPLICATION NUMBER: 60/063544
 ; PRIOR FILING DATE: 1997-10-28
 ; Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 612
 ; SEQ ID NO 347
 ; LENGTH: 3871
 ; TYPE: DNA
 ; ORGANISM: Homo Sapien
 US-10-199-670-347

Query Match	26.5%;	Score 718.6;	DB 13;	Length 3871;
Best Local Similarity	61.9%;	Pred. No. 7.4e-206;		
Matches 1233;	Conservative	0;	Mismatches 739;	Indels 21; Gaps 5
Qy	269	AATGGGAAGAACAATGTGCCAAGGCTGAAATATTCCTACAAGAAATGTCGAATCCAAAC	328	
Db	215	ACTTTGAAGCAAAATATTCCAAGACTCAAGCTAACCTACAAGACTTCTGCTTTCAAAAT	274	
Qy	329	AATGTGATCACTTTCAATGGCTTGGCCAAACAGCTCCAGTTATCATACCTTCTCTTTGGAT	388	
Db	275	AGCTGTATTCCTTTTGGGTTTCATCAAGAGACTGGATTTTCAAACCTCTTCTCTAGAT	334	
Qy	389	GAGGAACGGAGTAGCGCTGATGTTGGACCAAGGATCACATATTTTCAATTCGACCTGGTT	448	
Db	335	GAGGAAGAGGCGAGCGTCTCTTGGGAGCCAAAGACCACATCTTTTACTCAGTCTGGTT	394	
Qy	449	AA---TATCAAGAGATTTTCAAAAAGATGTGTGGCCAGATCTTACACAGAAGAGATGAA	505	
Db	395	GACTTAAACAAAATTTTAAAGATTTATTGGCCCTGCTGCAAGGAACGGGTGAATTA	454	
Qy	506	TGCAATGGCGCTGGAAGAAGACATCCTGAAAGAAATGTGCTATTAATTCATCAAGGTACTTAAG	565	
Db	455	TGTAATATAGCTGGGAAGATGCCAATAACAGAAATGTGCAAAATTTTCAACAGTACTTCAG	514	
Qy	566	GCATATAATCAGACTCACTTCTGACCTGTGGAAACGGGGCTTTTTCATCCAATTTGCACC	625	
Db	515	CCCTATAACAAAATCTACATATATGTGTGGAACCTGGAGCATTTTATCCAATATGTGGG	574	
Qy	626	TACATTGAAATGGACATCATCCTGGAGCAAAATATTTTAAAGCTGGAGAACTCAATTTT	685	
Db	575	TATATTGATCTTGGAGTCTACAGGAGGATATTTATTTCAAACCTAGACACACATAAATTG	634	
Qy	686	GAATAACGGCGCTGGGAAGAGTCCATATGACCCCTAAGCTGCTGACAGCATCCCTTTTAATA	745	
Db	635	GAGTCTGGCAGACTGAATATGTCCTTTCATCCTCAGCAGCCTTTTGTCTAGTAATGACA	694	
Qy	746	GATGGAAATTTATCTCTGGAACCTGCAGCTGAATTTTATGGGGCGAGACTTTTGTATCTTTC	805	

Db 1115 AGAAATCCTGTAGTATATGAGTCTTTACTACAACGAGCTCCATCTTCAAAGGCTCTGCT 1174
QY 1217 GTGTGTATGTATAGCATGATGATGAGAGGGTGTCTTCTTGTCCATATGCCACAGG 1276
Db 1175 GTTGTGTATAGCATGCTGATGATGAGAGGGTGTCTTCTTGTCCATATGCCATAG 1234
QY 1277 GATGACCCCAACTATCAATGGTGTCTTATCAAGGAAGAGTCCCTTATCCAGCGCCAGGA 1336
Db 1235 GAAAGTGCAGACCATCGTTGGGTGAGTATGATGGAGAATTCCTTATCCAGCGCTGCT 1294
QY 1337 ACTTGTCCAGCAAAACATTTG---GTGGTTTGTACTTACAAGACCTTCTCTGATGAT 1393
Db 1295 ACATGTCCAGCAAAACCTATGACCCACTGATTAAGTCCACCCGAGATTTTCCAGATGAT 1354
QY 1394 GTTATAACCTTTGCAAGAGTCAATCCAGCCATGTACAATCCAGTGTCTTCTATGAACAAT 1453
Db 1355 GTATCAGTTTCATAAGCGGCACCTGTGATGTATAGTCCGTATACCCAGTTCAGGA 1414
QY 1454 CGCCCAATAGTATCAAAACGGATGTAATTAATTCATTAATTTACAAATTTGTGTAGACGA 1513
Db 1415 GGACCAACCTTCAAGAGATCAATGTGGATTACAGACTGACACAGATAGTGTGGATCAT 1474
QY 1514 GTGGATGCAGAGATGCGACATGATGATGTTTATCGGAACAGATGTTGGGACCGTT 1573
Db 1475 GTCAATGCAAGATGCGCAGTACGATGTAATGTTTCTTGGAACAGATTTGGAACCTGTC 1534
QY 1574 CTTAAAGTATTTCAATTCCTAAGGAGACTTGGTATGATTTTAAAGAGAGTCTGCTGGAA 1633
Db 1535 CTCAAAGTGTGAGCATTTCAAAGGAAAAGTGG---AATATGGAAGAGTGTGCTGGAG 1591
QY 1634 GAAATGACAGTTTTCGGGAACCGACTGTATTTTTCAGCAATGAGACTTTCACATAGCAG 1693
Db 1592 GAGTGTGAGATTTCAAGCACTCATCAATCATCTTGAACATGGAATTTGCTCTGAAGCAG 1651
QY 1694 CAACAACATATATTTGTTTCAACGGCTGGGGTGGCCAGCTCCCTTTACACCGGTGTGAT 1753
Db 1652 CAACAATGTACATTTGTTCCCGAGATGATAGTTTCAGTCTCTCTGCAAGATGCCAC 1711
QY 1754 ATTTACGGAAGCGTGTGCTGAGTGTGCTCGCCGCGAGACCTTATGCTGTGGAT 1813
Db 1712 ACTTATGGGAAAGCTTGGCAGACTGTTGCTTGGCAGAGACCCCTACTGTGCTGGGAT 1771
QY 1814 GCTTGTGATGTTCTGCTGATTTTCCACTGCAAGAGACGCAAGAGCAGCAAGATATA 1873
Db 1772 GGAATGTGATGTTCTGATGATGCTCTTCTTCTTAAAGAGAGCTTAGACGCCAGATGTA 1831
QY 1874 AGAATGGAGACCCACTGACTGCTTTCAGACTTACACCATGATTAATCACCATGGCCAC 1933
Db 1832 AAATATGGCAGCCCAATCACCCAGTGTGGGACATCGAAGACAGCATTAGTCAATG---AA 1888
QY 1934 AGCCCTGAGAGAGATCATCTATGCTGTAGAGATAGTACACATTTTGGATGCAAT 1993
Db 1889 ACTGCTGATGAAAGGATTTTGGCATTTGAATTTAACTCAACCTTCTGGAATGTATA 1948
QY 1994 CGAAGTGCAGAGAGCGTGTCTTATTGGCAATTTCCAGAGCGCAAAATGAAGAGCGMAAA 2053
Db 1949 CTTAAATCCCAACAGCAACTATTAATGGTATATCCAGAGGTGAGGGGATGAGCATCGA 2008
QY 2054 GAAGAGATCAGATGATGATCATATCATCAGGACAGATCAAGGCTTCTGCTAGTGTAGT 2113
Db 2009 GAGGAGTTGAAGCCCGATGAAGAGATCATCAAAACGGAATATGGCTACTGATTCGAAGT 2068
QY 2114 CTACAACAGAGATTCAGGCAATTTACCTCTGCCATGCGGTGGAAACATGGGTTCATACAA 2173
Db 2069 TTGAGAGAGAGATTTCTGGGATGTATTACTGCAAGCCGAGGACACACTTTTCATCCAC 2128
QY 2174 ACTCTTTTAAAGTAAACCTGGAATGATGATGACACAGAGCATTTGGAAGAACTTTCTTAT 2233
Db 2129 ACCATAGTGAAGCTGACTTTGAATGTGATGAGATGAACAGATGGAATAATACCCAGAGG 2188
QY 2234 AAAGATGATGATG 2246
Db 2189 GCAGAGCATGAGG 2201

RESULT 12

US-10-205-890-347
; Sequence 347, Application US/10205890
; Publication No. US20040048334A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMERANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C519
; CURRENT APPLICATION NUMBER: US/10/205,890
; PRIOR FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 347
; LENGTH: 3871
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-205-890-347

Query Match 26.5%; Score 718.6; DB 13; Length 3871;
Best Local Similarity 61.9%; Pred. No. 7.4e-206;
Matches 1233; Conservative 0; Mismatches 739; Indels 21; Gaps 5;
QY 269 AATGGGAGAACATGTCCAGGCTGAATATTCCTCAAGAAATGTTGGATCCAC 328
Db 215 ACTTGAAGCAAAATATTCAGACTCAAGCTAACCTCAAGAGACTTGCTGCTTCAAT 274
QY 329 AATGTGATCACTTTCAATGGCTTGGCCAGCTCCAGTTATCATACCTTCTCTTTGGAT 388
Db 275 AGCTGATATCCCTTTTGGTTTCATCAGAGGACTGGATTTTCAAACTCTTCTTTAGAT 334
QY 389 GAGGAACGAGTAGGTGTATGTTGAGCAAGGATCAGATATTTTCATTCGACCTGGTT 448
Db 335 GAGGAAGAGGAGGCTGCTTGGGAGCCAAAGACCATCTTCTACTCTAGTCTGGTT 394
QY 449 AA---TATCAAGATTTTCAAAAGATTGTGTGCCAGTATCTTACACCAAGAGAGATGAA 505
Db 395 GACTTAAACAAATTTTAAAGAGATTTATTGGCTCTGCTCAAGAGAAACGGGTGGATTA 454
QY 506 TCGAAGTGGCTGGAAGACATCTCGAAGAGATGCTGTAATTTCAATCAAGGTAAG 565

Db 455 TGTAATAGTCTGGGAAAGATGCCAATACAGAAATGTGCAAAATTCATCAGAGTACTTCAG 514
Qy 566 GCATATAATCAGACTCAGCTGTACGCTGTGAAAGGGGGCTTTTCAATCAATTTGCAACC 625
Db 515 CCCTATAACAAACTCAGATATATGTGTGGAATCTGGAGCATTCATCCCATATGTGGG 574
Qy 626 TACATTGAATTTGGACATCATCTCTGAGGACATATATTTTATAGCTGGAGAACTCAGATTTT 685
Db 575 TATATTGATCTTGGAGCTCTCAAGGAGGATATATATTTCAAACTAGACACATATAATTTG 634
Qy 686 GAAACCGGCGTGGGAAAGTCCATATGACCCCTAAGCTGCTGACAGCATCCCTTTTAAATA 745
Db 635 GAGTCTGGCAGACTGAATGTCTTTTCGATCTCTGAGGCTTTTGTCTTCAGTATGACA 694
Qy 746 GATGGAGATTAATCTCTGGAATCTGAGCTGAGCTGATTTTATGGGCGGAGACTTTGCTATCTTC 805
Db 695 GATGAGTACTCTACTCTGGAACAGCTTCTGATTTCTTGGCAAGATACTGCAATTCAT 754
Qy 806 CGAACTCTTGGGC-----ACCACCCCAATCAGGACAGCAGCATGATTTCCAGG 856
Db 755 CGATCCCTTGGGCTACTCATGACCACTACATCAGACTGCAATTCAGAGCATAC 814
Qy 857 TGCGTAAATGATCCAAAGTTCAATAGTGGCCACCTCATCTCAGAGAGTGAATCTCTGAA 916
Db 815 TGSCCTCAATGGAGCAAAATTTATTTGGAATCTTCTTATACACAGACACCTCAATCCAGAT 874
Qy 917 GATGACAAAGTATATCTTTCTTCTGTAATGCAATGATGAGGAGACATCTCTGGAATA 976
Db 875 GATGATATAATATTTCTTCTTCTGTAATCATCTCAAGAGGAGTACTCTCGATATA 934
Qy 977 GCTACTCAGCTAGAAATAGTCAGATATGCAAGATGATCTTGGAGGCAAGAGCTG 1036
Db 935 ACCATCTTCTCGAGTGGAGAGTTTGTAAAGATGATGAGGAGGACAAAGGAGCTG 994
Qy 1037 GTCAATAATGGACAACTTCTCAAGCTCTGCTGATTTGCTCAGTCCAGGCTCCAAAT 1096
Db 995 ATAAACAAGTGGAGCTTTTCTTAAAGCCAGCTGATTTGCTCAATCTCTGGAGTAT 1054
Qy 1097 GGCATTGACACTCAATTTGATGAACTGAGGATGATTTCTTAATGAACTTTAAAGATCT 1156
Db 1055 GGGCGAGATCTTACTTTGATGCTTCAAGATATTTATTTACTCCCAAGAGATGAA 1114
Qy 1157 AAAAAATCCAGTGTATATGAGTGTATACGCTTCCAGTATCAATTTTCAAGGAGTACGCC 1216
Db 1115 AGAATCTGTAGTATATGAGTCTTTTACTACAAACAGCTCCATCTTCAAGGCTCTGCT 1174
Qy 1217 GTGTATGATATAGCATGATGATGAGAGGGTGTCTTGTGTCATATGCCCAAGG 1276
Db 1175 GTTTGTGTATAGCATGCTGACATCAGAGCAGTTTTTAATGGTCCATATGCTCATAAG 1234
Qy 1277 GATGGACCAACTATCAATGGTGTCTTATCAAGGAAGTCCCTATCCAGGCCAGGA 1336
Db 1235 GAAAGTGCAGACCATCTGTTGGTGCAGTATGATGGAGAAATCTTATCCAGGCTGTGT 1294
Qy 1337 ACTGTGCCAGCAAAACATTTG---GTGTTTTGACTCTCAAGAGACTTCTCTGATGAT 1393
Db 1295 ACATGTCCAAGCAAAACCTATGACCCACTGATTAAGTCCACCCGAGATTTTCCAGATGAT 1354
Qy 1394 GTTATAACCTTTGCAAGAGTATCATCAGCCATGTACAAATCCAGTGTCTTCTATGAACAAT 1453
Db 1355 GTCATCAGTTTCAATAGCGGCACTCTGTGATGATATAGTCCGTATACCCAGTTCAGGA 1414
Qy 1454 CGCCCAATAGTATCAAAACCGAGTAAATTAATTAATTAACAAATTTGCTAGACCGA 1513
Db 1415 GGACCAACGTTCAAGAGATCAATGTGGATTTACAGACTGACACAGATAGTGTGGATCAT 1474
Qy 1514 GTGGATGCAAGATGCAAGTATGATGTATGTTTTATCGGAAACAGATGTTGGACCGTT 1573
Db 1475 GTCAATTTGAGAGATGCGCAGTACGATGATGTTTTTCTTGGACAGACATTTGGACTGTC 1534
Qy 1574 CTTAAAGTATGTTCAATCTTAAAGAGACTTGGTATGATTTTAAAGAGGTTTCTCTCGAA 1633
Db 1535 CTCAAAAGTTGTGAGCATTTCAAGGAAAGAGTGG---AATATGGAGAGGAGTGTCTCTGGAG 1591

Qy 1634 GAAATGACAGTTTTTTCGGGAACCGAGCTGCTATTTTTCAGCAATGGAGCTTTCCACTAAGCAG 1693
Db 1592 GAGTTGAGATATTTCAAGCACTCATCAATCATCTTTGAACATGGAATTTGTCTCTGAAGCAG 1651
Qy 1694 CACCACTATATATTTGGTTTCAACGGCTGGGGTTCCCGAGCTCCCTTTTACACCGGTGTGAT 1753
Db 1652 CAACCAATTTGATTTGGTTTCCCGAGATGATTTGATTTGATCTCTCTTTCGACAGATGGAC 1711
Qy 1754 ATTACGGGAAAGCGTGTGCTGAGTGTTCCTCCCGGAGACCTCTTACTGTCTTGGGAT 1813
Db 1712 ACTTATGGGAAAGCTTTCGAGACTGTTGCTTTCGAGAGACCTCTACTGTGCTGGAT 1771
Qy 1814 GGTTCGATGTTCTCGCTATTTTCCCACTCAAGAGAGCGCAAGACGACAGATATA 1873
Db 1772 GAAATGCTGCTCTCGATATGCTCTTCTTCTTAAAGGAGAGCTAGACCCCAAGATGA 1831
Qy 1874 AGAATGAGAGACCCACTGACTCACTGTTTCACTTACACTTACACCATGATATCAACCATGGCCAC 1933
Db 1832 AATATGGCGACCCCAATCAACCCAGTGTGCGACATCGAAGACAGCATTTAGTCTATG---AA 1888
Qy 1934 AGCCCTGAAGAGAGATCATCTATGTTGTAGAGATAGTAGACATTTTGGATGCACT 1993
Db 1889 ACTGCTGATGAAAGGTGATTTTGGCATTTGAATTTAACTCAACCTTTCTGGATGTATA 1948
Qy 1994 CCGAAGTCCGAGAGAGCGCTGCTCTATTGGCAATTTCCAGAGGCGAAATGAAGAGCGAAAA 2053
Db 1949 CCTAATCCCAACAGCAACTATTAAATGTTATATCCAGAGGTCAGGGGATGAGCATCGA 2008
Qy 2054 GAAGAGTCAAGTGGATGATCATCATCAGGACAGATCAGGCTTCTGCTACGATG 2113
Db 2009 GAGGAGTTGAAGCCCGATGAAAGAAATCATCAAAACCGAATATGGGCTTACTGATTCGAAGT 2068
Qy 2114 CTACACAAAGAGGATTCAGGCAATTAAGTCTGCTGCTGCAATCGGTGGAACATGGGTTTATACAA 2173
Db 2069 TTGCAGAGAGAGGATTTCTGGATGATTTACTTGCAAAACCCAGGAGCACATTTTCAATCCAC 2128
Qy 2174 ACTTCTTATAGTAACTGGAAGTCAATGACAGAGCATTTTGGAGAACTTTCTTCAT 2233
Db 2129 ACCATAGTGAAGCTGACTTTGAATGTCAATGAGAAATGAACAGATGAAATATCCAGAGG 2188
Qy 2234 AAGAGTATGATG 2246
Db 2189 GCAGAGCATGAGG 2201

RESULT 13

US-10-208-024-347
; Sequence 347, Application US/10208024
; Publication No. US20040048335A1

GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3430R1C538

; CURRENT APPLICATION NUMBER: US/10/208,024

; PRIOR FILING DATE: 2002-07-29

; PRIOR APPLICATION NUMBER: 10/052586

; PRIOR FILING DATE: 2002-01-15

; PRIOR APPLICATION NUMBER: 60/059263

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/059266

; PRIOR FILING DATE: 1997-09-18

```

; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 347
; LENGTH: 3871
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-208-024-347

Query Match      26.5%; Score 718.6; DB 13; Length 3871;
Best Local Similarity 61.9%; Pred. NO. 7.4e-206;
Matches 1233; Conservative 0; Mismatches 739; Indels 21; Gaps 5

QY 269 AATGGGAAGAACAACTGCGCAAGGCTGAAATTATCCTCAAGAAAGAAATGTTGGAATCCAAAC 328
DB 215 ACTTTGAGCAAAATATTTCCAGACTCAAGCTAACTCAACAGACTTGTGCTTCCAAT 274

QY 329 AATGTGATCACTTTCAATGGCTTGCCCAACAGCTCCAGTTATCATACCTTCCTTTTGGAT 388
DB 275 AGCTGTATTCCTTTTGGGTTTCATCAGAAGACTGGATTTTCAAACTCTCTCTTAGAT 334

QY 389 GAGGAACGAGTAGGCTGTATGTTGGAGCAAGAGATCACATATTTTCATTCGACCTGGTT 448
DB 335 GAGGAAGAGGAGGAGGCTGCTCTTGGGAGCCAAAGACCACATCTTTCTACTCAGTCTGGTT 394

QY 449 AA---TATCAAGGATTTTCAAAAGATTGTGTGGCCAGTACTCTTACACCAGAAGAGATGAA 505
DB 395 GACTTAAACAAAAATTTTAAGAGATTATTTGGCCTGCTGCAAGGACGGGTGGAATTA 454

QY 506 TGCAGTGGGCTGGAAAAGACATCTCGAAAGATGTGCTTAATTTCACTAAGGTACTTAAG 565
DB 455 TGTAAATTAGCTGGGAAAGATGCCAATACAGAATGTGCAAAATTCATCAGAGTACTTCAG 514

QY 566 GCATATAATCAGACTCACTGTGACGCTGTGGAACGGGGGCTTTTCATCCAAATTTGCACC 625
DB 515 CCTTATACAAAATCTCAATATGTGTGTGGAATCTGGAGCATTTTATCCAAATATGTGGG 574

QY 626 TACATTGAAATTGGACATCATCCTGAGGACAAATATTTTAAAGCTGGAGAACTCACATTTT 685
DB 575 TATATTGATCTTTGGAGTCTCAAGGAGGATATTATATTCAAACCTAGACACACATAATTTG 634

QY 686 GAAACGGCCGTGGGAAGAGTCCATATGACCCCTAAGCTGTGACAGCATCCCTTTTAATA 745
DB 635 GAGTCTGGCAGACTGAAATGTCCTTCATGCTCCTCAGCAGCCTTTTGTCTTCAGTAATGACA 694

QY 746 GATGGAGAATTATCTCTTGGAACTGCAGCTGATTTTATGGGGCGAGACTTTTGCTATCTTC 805
DB 695 GATGAGTACCTCTACTCTTGGAAACAGCTTCATGATTTCTTGGCAAGATACTGCAATTCAC 754

QY 806 CGAACTCTTTGGGC-----ACCAACCCCAATCAGGACAGAGCATGATTCACGG 856
DB 755 CGATCCCTTTGGGCCTACTCATGACCACCACCTACATCAGAACTGCACATTTTCAGHAGCACTAC 814

QY 857 TGSGCTCAATGATCCAAAGTTCAATAGTGCCCACTCATCTCAGAGAGTGACAACTCTCGAA 916
DB 815 TGSGCTCAATGGAGCAAAATTTATTTGGAACTTTCTTCTCATACAGACACCTACATCCAGAT 874

QY 917 GATGACAAAGTATATCTTTTCTTCGGTGAATAATGCAATAGATGGAGAAACATCTCGAAAA 976
DB 875 GATGATAAAATATATTTCTTTTCGTTGAACTCATCTCAAGAAAGCAGTACTCCGATAAA 934

```

QY 2054 GAAGAGATCAGATGGATGATCATATCATCAGGACAGATCAAGGCTTCTGCTACGTTAGT 2113
DB 2009 GAGGAGTTGAAGCCGATGAAGAATCATCAAAACGGAATATGGGCTTACTGATTCGAGT 2068
QY 2114 CTACACAGAAGGATTCAGGCAATTAACCTCTGCCATCGGTTGGAACATCGGTTTCATCAA 2173
DB 2069 TTGAGAGAGAGGATCTGGGATGTATTAATGCAAGCCAGGAGGACACATTTTCATCCAC 2128
QY 2174 ACTCTTTTAAAGTTAAACCTCGGAAGTATTCACACAGAGCATTTGGAAGAACTTCTTCAT 2233
DB 2123 ACCATAGTGAAGCTGACTTTGAATCTCATTCAGAAATGAACAGATGGAAGAAATACCCAGAG 2188
QY 2234 AAAGATGATGATG 2246
DB 2189 GCAGAGCATGAGG 2201

RESULT 14
US-10-201-853-347
; Sequence 347, Application US/10201853
; Publication No. US20040053358A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C465
; CURRENT APPLICATION NUMBER: US/10/201,853
; PRIORITY FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 347
; LENGTH: 3871
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-201-853-347

Query Match 26.5%; Score 718.6; DB 13; Length 3871;
Best Local Similarity 61.9%; Pred. No. 7.4e-206;
Matches 1233; Conservative 0; Mismatches 739; Indels 21; Gaps 5;

QY 269 AATGGGAAGCAATGTCGAGGCTGAATATCTACAAAGAAATCTTGAATCCCAAC 328
DB 215 ACTTTGAAGCAAAATATTCAGAGACTCAAGCTAACTACAAAGAACTTGTCTGCTTTCAAT 274

QY 329 AATGTGATCACATTTCAATGGCTTGGCCAAACAGCTCCAGTTATCATACCTCTCTTTTGGAT 388
DB 275 AGCTGTATTCCTTTTGGGTTTCATCAGAGACTGGATTTTCAAACTCTTCTCTTAGAT 334
QY 389 GAGGAACGGAGTGTATGTGTGGAGCAAGGATCATATTTTCAATTCAGACTGGTT 448
DB 335 GAGGAAGAGGCGAGCTGTCTTGGGAGCCAAAGACCACTCTTTTACTCAGTCTGGTT 394
QY 449 AA---TATCAAGGATTTTCAAAAGATTGTGTGGCCAGTATCTTACCCAGAGAGATGAA 505
DB 395 GACTTAACAAGAAATTTAAGAGATTTATTTGGCTGTCTCAAGGACGGGTGAATTA 454
QY 506 TGCAAGTGGCTGGAAAGACATCTCTGAAAGATGTGTCTTAATTTTCAATCAAGACTTAAG 565
DB 455 TGTAAATTAGCTGGGAAAGATGCCAATACAGAAATGTCAAAATTTTCAATCAGAGTACTTCAG 514
QY 566 GCATATATCAGACTCACTTGTACGCTGTGGAACGGGGCTTTTCAATCCAAATTTGCACC 625
DB 515 CCTATAACAAACTCACATATATGTGTGGACTGGAGCATTTTCAATCAATATGTGG 574
QY 626 TACATTTGAAATTTGGACATCATCTCTGAGGACATATTTTAAAGCTGGAGAACTCAATTTT 685
DB 575 TATATTGATCTTGGAGTCTTCAAGGAGGATATTAATTTCAAACTAGACACACATAATTTG 634
QY 686 GAAAACGGCGTGGGAAGTCCATATGACCTAGCTGCTGACAGCATCTCTTTTAATA 745
DB 635 GAGTCTGGCAGACTGAAATGTCTTTTCGATCTCTGAGGCTTTTGTCTTCAAGTATGACA 694
QY 746 GATGGAGATTAATACTCTGGAATCTGAGTGTATTTATGGGCGGAGACTTTGCTATCTTC 805
DB 695 GATGAGTACTCTACTCTGGAACGCTTCTGATTTCCITGGCAAGATATGCAATCACT 754
QY 806 CGAATCTTTGGGC-----ACCAACCCAACTCAGACAGACAGCATGATTCAGG 856
DB 755 CGATCCCTTTGGGCTTACTCATGACCACCACTACATCAGAACTGACATTTTCAAGAGCACTAC 814
QY 857 TGGCTCAATGATCCAAAGTTCATTAGTGCCACCTCATCTCAGAGAGTGACAAATCCTCAA 916
DB 815 TGGCTCAATGAGGAGCAAAATTAATGGAATTTCTTCTACACAGACACCTACATCCAGAT 874
QY 917 GATGACAAAGTATATCTTTTCTTCCGTGAAATGCAATAGATGAGGAGACATCTCTGAAA 976
DB 875 GATGATAAAATATATTTCTTCTTCTGTAATCATCTCAAGAGGCGAGTACCTCCGATAA 934
QY 977 GCTACTCAGCTAGATAGGTGAGATATGCAAGATGATTTGGAGGGGACAGAGAGTCTG 1036
DB 935 ACCATCTTTCTCGAGTTGGAAAGATTTGTAGAATGATGTAGGAGGACAGCGAGCTG 994
QY 1037 GTGAATAAATGGACAAACATTTCTCAAGCTCGTCTGATTTGCTCAGTGCAGGTCCAAAT 1096
DB 995 ATAAACAGAGTGGAGCGACTTTCTTAAGGCCAGACTGATTTGCTCAATTCCTGGAAGTGT 1054
QY 1097 GGCATTTGACATCATTTTCAATGAGTGTATCTTCTTAATGATGATTTTAAAGATCT 1156
DB 1055 GGGCGAGATATCTTACTTGTGAGCTTCAAGATATTTATTCTCCCAACAGAGATGAA 1114
QY 1157 AAAAATCCAGTTGTATATGAGTGTATGAGCTTCCAGTAAACATTTTCAAGGGATCAGCG 1216
DB 1115 AGAAATCTGTAGTATATGAGTCTTTTACTAACACAGCTCCATCTTCAAGGGCTCTGCT 1174
QY 1217 GTGTGTATGTATAGCATGATGTAGTGAAGAGGTTCTCTTGGTCCATATSCCAGG 1276
DB 1175 GTTTGTGTATAGCATGCTGACATCAGAGCAGTTTTAAATGGTCCATATGCTCATAG 1234
QY 1277 GATGGACCCAACTATCAATGGGTGCTTATCAAGGAAGAGTCCCTTATCCAGGGGACAGA 1336
DB 1235 GAAAGTGCAGACCATCGTTGGGTGAGTATGATGGAGAAATTCCTTATCCAGGCTGT 1294
QY 1337 ACTTGTCCCAGCAAAACATTTG---GTGTTTGTAGCTTACAAAGACCTTCTGTATGAT 1393
DB 1295 ACATGTCCAAGCAAAACCTATGACCACCTGATTAAGTCCACCCGAGATTTTCCAGATGAT 1354

1394 GTTATAACCTTTGCAAGAAGTCCATCCAGCCATGACAAATCCAGTGTCTTCTATGAACAAT 1453
1395 GTTCATCAGTTTCATTAAGCGGCACTCTGTGATGATATAGTCCGTATACCCAGTTCGAGGA 1414
1454 CCCCCAATAGTATGATCAAAACGGATGTAATATCAATTTACAAATTTGTCGTAGACCGA 1513
1415 GGACCAACGGTTCAAGAGAATCAATGTGATTCACAGATGACACAGATAGTGTGGATCAT 1474
1514 GTGGATGACAGAGATGGACAGTATGATGTATGTTTATCGGAACAGATGTTGGGACCGTT 1573
1475 GTCAATGCAAGATGCGCCAGTACGATGATGTTTCTTGAACAGACATTTGGAACTGTC 1534
1574 CTTAAAGTAGTTTCAATTCCTAAGGAGACTTGGTATGATTTAGAAAGGTTCTGCTGAAA 1633
1535 CTCAAAGTTGTGAGCATTTCAAAGGAAAAGTGG---AATATGGAAGAGGTAGTGTGGAG 1591
1634 GAAATGACAGTTTTCGGGACCGACTGCTATTTTCAGCAATGGAGCTTTCACATGAAGAG 1693
1592 GAGTTGCGAGATTTCAAGCACTCATCAATCATCTTGAACATGGAATGTTCTCTGAAGAG 1651
1694 CAACAACATATATTTGGTTTCAACGGCTGGGTTGCCAGCTCCCTTTACACCGGTGTGAT 1753
1652 CAACAATTCATATTTGGTTCCGAGATGATTTAGTTCAGCTCTCCTTCACAGATGCGAC 1711
1754 ATTTAGGGAAGCGTGTGCTGAGTGTGCTCGCCCGAGACCTTACTGTGCTTGGAT 1813
1712 ACTTATGGGAAAGCTTGGCAGACTGTTGTCTTGGCAGAGACCCCTACTGTGCTCGGAT 1771
1814 GGTTCGTGATGTTCTGCTATTTTCCCACTGCAAGAGACGCAAGACGCAAGATATA 1873
1772 GGAATGATGCTCTCGATGCTCTTCTTCTTAAAGGAGAGCTAGAGCGCCAGATGTA 1831
1874 AGAATGGAGACCCACTGACTCACTGTTTCACTTACACCATGATGATCAATCAGTGGCCAC 1933
1832 AAATATGGGACCCCAATCAACCCAGTCTGGGACATCGAAGACAGCATTTAGTCATG---AA 1888
1934 AGCCCTGAAGAGAGATCATCTATGTTGATAGATAGTAGACATTTTGGATGCGAGT 1993
1889 ACTGCTGATGAAGAGTATTTTGGCATGTAATTTAACTCAACCTTCTGGAATGATA 1948
1994 CCGAAGTCGACAGAGCGCTGCTTATTGGCAATTCAGAGCGGAAATGAAGAGCGAAA 2053
1949 CTTAAATCCCAACAGCAACTATTAATGGTATATCCAGAGTTCAGGGGATGAGCATCGA 2008
2054 GAAGAGATCAGATGATGATCATATCATCAGGACAGATCAAGGCTTCTGCTAGTGTAGT 2113
2009 GAGGAGTTGAAGCCCGATGAAAGAAATCATCAAAACGGAATATGGGCTACTGATTCGAAGT 2068
2114 CTACACAGAGAGATTCAGGCAATACCTCTGCCATGCGGTGGAACATGGGTTCATACAA 2173
2069 TTGCAGAGAGAGATTTCTGGGATGATTTACTGCAAGCCAGGAGCACACTTTCATCCAC 2128
2174 ACTTCTTTAAGTAACTTGAAGTATGATGACAGAGCATTTGGAAGAACTTTCTTCAT 2233
2129 ACCATAGTGAAGTGACTTTGAATGTGATGATGAAATGAACAGATGGAATAACCCAGAGG 2188
2234 AAGATGATGATG 2246
2189 GCAGAGCATGAGG 2201

RESULT 15

US-10-174-581-347
; Sequence 347, Application US/10174581
; Publication No. US20030017540A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James

APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430R1C41
CURRENT FILING DATE: 2002-06-18
CURRENT APPLICATION NUMBER: US/10/174,581

PRIOR APPLICATION NUMBER: 10/052586
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063120
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063121
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063486
PRIOR FILING DATE: 1997-10-21
PRIOR APPLICATION NUMBER: 60/063540
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063541
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063544
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063564
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063734
PRIOR FILING DATE: 1997-10-29
PRIOR APPLICATION NUMBER: 60/063870
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066120
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/066466
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/066772
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/069335
PRIOR FILING DATE: 1997-12-11
PRIOR APPLICATION NUMBER: 60/069425
PRIOR FILING DATE: 1997-12-12
PRIOR APPLICATION NUMBER: 60/069870
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/068017
PRIOR FILING DATE: 1997-12-18
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078939
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079664
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079786
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/080107
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080194
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080327
PRIOR FILING DATE: 1998-04-01

/ PRIOR APPLICATION NUMBER: 60/080333
 / PRIOR FILING DATE: 1998-04-01
 / PRIOR APPLICATION NUMBER: 60/081049
 / PRIOR FILING DATE: 1998-04-08
 / PRIOR APPLICATION NUMBER: 60/081070
 / PRIOR FILING DATE: 1998-04-08
 / PRIOR APPLICATION NUMBER: 60/081195
 / PRIOR FILING DATE: 1998-04-09
 / PRIOR APPLICATION NUMBER: 60/081838
 / PRIOR FILING DATE: 1998-04-15
 / PRIOR APPLICATION NUMBER: 60/082568
 / PRIOR FILING DATE: 1998-04-21
 / PRIOR APPLICATION NUMBER: 60/082569
 / PRIOR FILING DATE: 1998-04-21
 / PRIOR APPLICATION NUMBER: 60/082704
 / PRIOR FILING DATE: 1998-04-22
 / PRIOR APPLICATION NUMBER: 60/082797
 / PRIOR FILING DATE: 1998-04-22
 / PRIOR APPLICATION NUMBER: 60/083322
 / PRIOR FILING DATE: 1998-04-28
 / PRIOR APPLICATION NUMBER: 60/083495
 / PRIOR FILING DATE: 1998-04-29
 / PRIOR APPLICATION NUMBER: 60/083496
 / PRIOR FILING DATE: 1998-04-29
 / PRIOR APPLICATION NUMBER: 60/083499
 / PRIOR FILING DATE: 1998-04-29
 / PRIOR APPLICATION NUMBER: 60/083559
 / PRIOR FILING DATE: 1998-04-29
 / PRIOR APPLICATION NUMBER: 60/084366
 / PRIOR FILING DATE: 1998-05-05
 / PRIOR APPLICATION NUMBER: 60/084414
 / PRIOR FILING DATE: 1998-05-06
 / PRIOR APPLICATION NUMBER: 60/084639
 / PRIOR FILING DATE: 1998-05-07
 / PRIOR APPLICATION NUMBER: 60/084640
 / PRIOR FILING DATE: 1998-05-07
 / PRIOR APPLICATION NUMBER: 60/084643
 / PRIOR FILING DATE: 1998-05-07
 / PRIOR APPLICATION NUMBER: 60/085573
 / PRIOR FILING DATE: 1998-05-15
 / PRIOR APPLICATION NUMBER: 60/085579
 / PRIOR FILING DATE: 1998-05-15
 / PRIOR APPLICATION NUMBER: 60/085580
 / PRIOR FILING DATE: 1998-05-15
 / PRIOR APPLICATION NUMBER: 60/085582
 / PRIOR FILING DATE: 1998-05-15
 / PRIOR APPLICATION NUMBER: 60/085700
 / PRIOR FILING DATE: 1998-05-15
 / PRIOR APPLICATION NUMBER: 60/086023
 / PRIOR FILING DATE: 1998-05-18
 / PRIOR APPLICATION NUMBER: 60/086392
 / PRIOR FILING DATE: 1998-05-22
 / PRIOR APPLICATION NUMBER: 60/086486
 / PRIOR FILING DATE: 1998-05-22
 / PRIOR APPLICATION NUMBER: 60/087098
 / PRIOR FILING DATE: 1998-05-28
 / PRIOR APPLICATION NUMBER: 60/087208
 / PRIOR FILING DATE: 1998-05-28
 / PRIOR APPLICATION NUMBER: 60/087609
 / PRIOR FILING DATE: 1998-06-02
 / PRIOR APPLICATION NUMBER: 60/087759
 / PRIOR FILING DATE: 1998-06-02
 / PRIOR APPLICATION NUMBER: 60/087827
 / PRIOR FILING DATE: 1998-06-03
 / PRIOR APPLICATION NUMBER: 60/088025
 / PRIOR FILING DATE: 1998-06-04
 / PRIOR APPLICATION NUMBER: 60/088028
 / PRIOR FILING DATE: 1998-06-04
 / PRIOR APPLICATION NUMBER: 60/088029
 / PRIOR FILING DATE: 1998-06-04
 / PRIOR APPLICATION NUMBER: 60/088033
 / PRIOR FILING DATE: 1998-06-04
 / PRIOR APPLICATION NUMBER: 60/088167

/ PRIOR FILING DATE: 1998-06-05
 / PRIOR APPLICATION NUMBER: 60/088202
 / PRIOR FILING DATE: 1998-06-05
 / PRIOR APPLICATION NUMBER: 60/088212
 / PRIOR FILING DATE: 1998-06-05
 / PRIOR APPLICATION NUMBER: 60/088217
 / PRIOR FILING DATE: 1998-06-05
 / PRIOR APPLICATION NUMBER: 60/088326
 / PRIOR FILING DATE: 1998-06-04
 / PRIOR APPLICATION NUMBER: 60/088655
 / PRIOR FILING DATE: 1998-06-09
 / PRIOR APPLICATION NUMBER: 60/088722
 / PRIOR FILING DATE: 1998-06-10
 / PRIOR APPLICATION NUMBER: 60/088738
 / PRIOR FILING DATE: 1998-06-10
 / PRIOR APPLICATION NUMBER: 60/088740
 / PRIOR FILING DATE: 1998-06-10
 / PRIOR APPLICATION NUMBER: 60/088811
 / PRIOR FILING DATE: 1998-06-10
 / PRIOR APPLICATION NUMBER: 60/088824
 / PRIOR FILING DATE: 1998-06-10
 / PRIOR APPLICATION NUMBER: 60/088825
 / PRIOR FILING DATE: 1998-06-10
 / PRIOR APPLICATION NUMBER: 60/088826
 / PRIOR FILING DATE: 1998-06-10
 / PRIOR APPLICATION NUMBER: 60/088861
 / PRIOR FILING DATE: 1998-06-11
 / PRIOR APPLICATION NUMBER: 60/088863
 / PRIOR FILING DATE: 1998-06-11
 / PRIOR APPLICATION NUMBER: 60/088876
 / PRIOR FILING DATE: 1998-06-11
 / PRIOR APPLICATION NUMBER: 60/089090
 / PRIOR FILING DATE: 1998-06-12
 / PRIOR APPLICATION NUMBER: 60/089105
 / PRIOR FILING DATE: 1998-06-12
 / PRIOR APPLICATION NUMBER: 60/089512
 / PRIOR FILING DATE: 1998-06-16
 / PRIOR APPLICATION NUMBER: 60/089514
 / PRIOR FILING DATE: 1998-06-16
 / PRIOR APPLICATION NUMBER: 60/089538
 / PRIOR FILING DATE: 1998-06-17
 / PRIOR APPLICATION NUMBER: 60/089598
 / PRIOR FILING DATE: 1998-06-17
 / PRIOR APPLICATION NUMBER: 60/089653

Query Match 26.5%; Score 718.6; DB 13; Length 3871;
 Best Local Similarity 61.9%; Pred. No. 7.4e-206;
 Matches 1233; Conservative 0; Mismatches 739; Indels 21; Gaps 5;

QY 269 AATGGGAAGAACAAATGTCGAAGGCTGAATATCTTACAAAGAAATGTTGGAATCCAC 328
 DB 215 ACTTTGAAGCAAAATATTCGAAGCTCAAGCTAACCTACAAAGACTTGCTGCTTTCAAT 274
 QY 329 AATGTGATCACTTCAATGCTTGCCCAACAGCTCCAGTTATCATACCTTCCTTTTGGAT 388
 DB 275 AGCTGTATTCCTTTTGGGTTCAATCAGAGACTGGATTTTCAACTCTTCTTAGAT 334
 QY 389 GAGGAACGGAGTAGGCTGTATGTTGAGCAAAAGGATCACATATTTTCACTGACCTGGTT 448
 DB 335 GAGGAAGAGGCGAGGCTGCTCTTGGAGCCAAAGACCATCTTTCTACTAGTCTGGTT 394
 QY 449 AA---TATCAAGGATTTTCAAAAGATTTGTCGCGAGTATCTTACACCAAGAGAGATGAA 505
 DB 395 GACTTAAACAAAATTTTAAAGAGATTTATTGGCTGCTGCAAGGACGGGTGGAATTA 454
 QY 506 TGAAGTGGGCTGGAAGAACATCTCTGAAAGAAATGTGCTAAATTTTCAAGTACTTAAG 565
 DB 455 TGTAATATTAGTGGGAAGAGATGCCAATACAGAAATGTGCAATTTTCACTAGACTTTCAG 514
 QY 566 GCATATAATCAGACTCACTGTGACGCTGTGGAACGGGGCTTTTCATCCCAATTTGCACC 625
 DB 515 CCTATAACAAAACACTCACATATATGTGTGGAACCTGGAGCAATTTTCAATCAATATGTGG 574

QY 626 TACATTGAAATTGGACATCATCTGAGGACAAATATTTTAAAGCTGGAGAACTCACAATTTT 685
Db 575 TATATTGATCTTGGAGCTCAAGGGAGATATATATTCNAACTAGACACACATATTTTG 634
QY 686 GAAAACGGCGTGGGAAGAGTCCATATGACCCTAAGCTGCTGACAGCATCCCTTTTAATA 745
Db 635 GAGTCTGGCAGACTGAAATGCTCTTGGATCCTCAGCAGCCTTTTGCCTCAGTAATGACA 694
QY 746 GATGGAGATATATCTCGGAACCTCAGCTGATTTTATGGGGGAGACTTTGCTATCTTC 805
Db 695 GATGAGTACCTCTACTCTGGAACAGCTTCTGATTTCTTGGCAAGATAGTGCATTCAC 754
QY 806 CGAACTCTTTGGGC-----ACCACCAACCAATCAGGACAGACAGCATGATTCACGG 856
Db 755 CGATCCCTTTGGGCTACTCATGACCACCACTACATCAGAAGTGCATTCAGAGCACTAC 814
QY 857 TGGCTCAATGATCCAAAGTTCATTAGTGCACCTCACTCAGAGAGTGACAACTCCTGAA 916
Db 815 TGGCTCAATGGAGCAAAATTTATGGAACTTTCTTCATACCAGACACCTTACAATCCAGAT 874
QY 917 GATGACAAAGTATATCTTTTCTTCGTGAAAATGCAATAGATGGAGAACACTCTCGAAAA 976
Db 875 GATGATAAATATATTTCTTTCTGTAATCATCTCAAGAGGCGAGTACCTCCGATAA 934
QY 977 GCTACTCAGCTAGAAATAGGTGAGATATGCAAGATGACTTTGGAGGGGACAGAACTGTG 1036
Db 935 ACCATCCCTTTCGAGTTGGAAGAGTTTGTAAAGATGATGTAGAGGAGCAACGCGACCTG 994
QY 1037 GTGAATAAATGACAACTTCTCAAAGCTGCTGATTTGCTCAGTGCAGGTCGAGTCCAAAT 1096
Db 995 ATAAACAAGTGGACGACTTTCTTAAGGCCAGCTGATTTGCTCAATTCCTTGGAAAGTAT 1054
QY 1097 GGCATTGACACTCAITTTGATGAAGTGCAGAGTATTCCTTAATGAAGCTTTAAAGATCCT 1156
Db 1055 GGGGCAGATACTTACTTTGATGAGCTTCAAGATATTTATTTACTCCCCACAGAGATGAA 1114
QY 1157 AAAATCCAGTTGTATATGGAGTGTACGACTTCCAGTAACTTTTCAGGGATCAGCC 1216
Db 1115 AGAAATCCCTGTAGTATGAGTGTCTTTACTACAAACGAGTCCATCTTCAAGAGCTCTGCT 1174
QY 1217 GTGTGTATGTATAGCATGATGATGTGAGAGGGTGTTCCTTGGTCCATATGCCACAGG 1276
Db 1175 GTTTGTGTATAGCATGCTGACATCAGAGCAGTTTAAATGGTCCATATGCTCATAG 1234
QY 1277 GATGGACCAACTATCAATGGGTGCTTATCAGAGAGTCCCTTATCCAGGGCCAGGA 1336
Db 1235 GAAAGTGCAGACCATCGTTGGGTGCGATGATGAGGAGAAATTCCTTATCCAGCGCTGCT 1294
QY 1337 ACTTGTCCAGCAAAACATTTG---GTGGTTTTGACTCTACAAAGAGCCTTCTCTGATGAT 1393
Db 1295 ACATGTCCAGCAAAACCTATGACCACATGATTAAGTCCACCCGAGATTTTCCAGATGAT 1354
QY 1394 GTTATAACCTTTGCAAGAGTCAATCCAGCCATGTACAAATCCAGTGTTCCTATGAACAAT 1453
Db 1355 GTCATCAGTTTCATAAAGCGGCACTGTGTGATGTATAGTCCGTATACCCAGTTGCAGGA 1414
QY 1454 CGCCCAATAGTATCAAAACGGATGTAAATTTCAATTTACAAATTTGCTGTAGACCGA 1513
Db 1415 GGACCAACGTTCAAGAGATCAATGGGATTAAGACTCAGACTCAGACAGATAGTGTGATCAT 1474
QY 1514 GTGGATGCAGAGATGGACAGTATGATGTATGTTTATCGGAACAGATGTTGGGACCGTT 1573
Db 1475 GTCATTTGAGAGATGCGCCAGTACGATGTAAATGTTTCTTGGAAACAGACATTGGAAGTGC 1534
QY 1574 CTTAAAGTAGTTTCAATTCCTAAGGAGACTTGGTATGATTTAGAGAGGTTCTGCTGGAA 1633
Db 1535 CTCAAAGTTTGTACAGCAATTTCAAAGGAAAAGTGG---AATATGGAAGAGTAGTGTGGAG 1591
QY 1634 GAAATCACAGTTTTTTCGGAAACCGACTGCTATTTTCAAGCAATGGAGCTTTCCACTAAGCAG 1693
Db 1592 GAGTTGCAGATATTCAAGCACTCATCAATCATCTTGAACATGGAATTTGCTCTGAGCAG 1651
QY 1694 CAACAACATATATATTTGGTTCAACGGCTGGGGTTGCCAGCTCCCTTTTACACCGGTGTGAT 1753

Db 1652 CAACAATTGTACATTTGTTTCCCGAGATGGATTAGTTTCCAGCTCTCTTTCGACAGATGCGAC 1711
QY 1754 ATTTACGGGAAAGGCTGTGCTGAGTGTTCCTGCGCCGAGACCTTACTGTGCTGGGAT 1813
Db 1712 ACTTATGGGAAAGCTTCCGAGACTGTGTCTTTTGGCCAGAGACCTTACTGTGCTGGGAT 1771
QY 1814 GGTTCCTCATGTTTCTCGCTATTTTCCCACTGCAAAAGAGAGCGCACAGACGACAAAGATATA 1873
Db 1772 GGAATGCTATGCTCTCGATATGCTCTTCTTCTTAAAGGAGAGTAGACGCCAAGATGTA 1831
QY 1874 AGAAATGGAGACCCACTGACTCTGTTTCAAGCTTACCATGATTAATCACTATGAGCCAC 1933
Db 1832 AAATATGGCAGCCCAATCACCCAGTCTGGGACATCGAAGACAGCAATTAGTCATG---AA 1888
QY 1934 AGCCCTCAAGAGAGAAATCATCTATGTTGTAGAGAAATAGTAGCACATTTTGGAAATGCAAT 1993
Db 1889 ACTGCTGATGAAGAGTGAATTTTGGCATTTGAATTTTAACTCAACCTTTCTGGAAATGATA 1948
QY 1994 CCGAAGTCGAGAGAGCGCTGTCTATTTGGCAATTTCCAGAGGCGAAATGAAGAGCGAAAA 2053
Db 1949 CCTAAATCCCAACAAGCAACTATTAAATGGTATATCCAGAGGTCAGGGGATGAGCATCGA 2008
QY 2054 GAAGAGATCAGAGTGGATGATCATATCATCAGACAGATCAAGGCTTCTGTCTACGTAGT 2113
Db 2009 GAGGAGTTGAAGCCCGGATGAAGAAATCATCAAAACCGGAATATGGGCTACTGATTCGAAGT 2068
QY 2114 CTACAAACAGAGAGATTCAGGCAATTAACCTCTGCCATGCGGTGGAAACATGGGTTTCATACAA 2173
Db 2069 TTGCAGAGAGAGGATTTCTGGGATCTATTACTGCAAAAGCCCGAGGACACACTTTTCATCCAC 2128
QY 2174 ACTCTTCTTAAGGTAAACCTGGAAGTCAATTTGACAGAGCATTTTGGAAAGAACTTCTTCAT 2233
Db 2129 ACCATAGTGAAGCTGACTTTTGAATGTCAATTGAGAAATGAACAGATGGAAAAATACCCAGAG 2188
QY 2234 AARGATCATGATG 2246
Db 2189 GCAGAGCATGAGG 2201

Search completed: September 23, 2004, 05:07:03
Job time : 1260 secs

This Page Blank (uspio)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 22, 2004, 23:37:55 ; Search time 194 Seconds
(without alignments)
7749.288 Million cell updates/sec

Title: US-09-774-490-1

Perfect score: 2709
Sequence: 1 aatcttttttttcgatg.....aggcttttttttcctaataacc 2709

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA: *
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq: *
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq: *
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq: *
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq: *
5: /cgn2_6/ptodata/2/ina/PTUS_COMB.seq: *
6: /cgn2_6/ptodata/2/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2508.4	92.6	2601	1 US-08-121-713D-53	Sequence 53, Appl
2	2508.4	92.6	2601	1 US-08-835-268-53	Sequence 53, Appl
3	2508.4	92.6	2601	3 US-09-060-692-53	Sequence 53, Appl
4	2508.4	92.6	2601	3 US-08-833-391-53	Sequence 53, Appl
5	2508.4	92.6	2601	4 US-09-060-610-53	Sequence 53, Appl
6	2508.4	92.6	2601	5 PCT-US94-10151A-53	Sequence 53, Appl
7	1415.2	52.2	1481	1 US-08-136-922-1	Sequence 1, Appl
8	596.4	22.0	2898	4 US-09-308-179B-2	Sequence 2, Appl
9	125	4.6	2278	4 US-09-976-594-1002	Sequence 1002, Ap
10	95.2	3.5	3692	4 US-09-077-940A-1	Sequence 1, Appl
11	90.6	3.3	1923	4 US-09-653-274-12	Sequence 12, Appl
12	90.6	3.3	3261	4 US-09-653-274-5	Sequence 5, Appl
13	90.6	3.3	3694	4 US-09-653-274-3	Sequence 3, Appl
14	84	3.3	2433	4 US-09-300-958A-24	Sequence 24, Appl
15	83.2	3.1	4157	4 US-08-556-422A-1	Sequence 1, Appl
16	69.8	2.6	2854	1 US-08-121-713D-57	Sequence 57, Appl
17	69.8	2.6	2854	1 US-08-835-268-57	Sequence 57, Appl
18	69.8	2.6	2854	2 US-09-060-692-57	Sequence 57, Appl
19	69.8	2.6	2854	3 US-08-833-391-57	Sequence 57, Appl
20	69.8	2.6	2854	4 US-09-060-610-57	Sequence 57, Appl
21	69.8	2.6	2854	5 PCT-US94-10151A-57	Sequence 57, Appl
22	68.4	2.5	2790	4 US-09-254-594-5	Sequence 5, Appl
23	68.4	2.5	3432	4 US-09-254-594-4	Sequence 4, Appl
24	60.6	2.2	3524	4 US-09-077-940A-3	Sequence 3, Appl
25	58.6	2.2	7218	1 US-08-232-463-14	Sequence 14, Appl
26	58.4	2.2	3560	1 US-08-121-713D-59	Sequence 59, Appl
27	58.4	2.2	3560	1 US-08-835-268-59	Sequence 59, Appl

Query Match 92.6%; Score 2508.4; DB 1; Length 2601;
Best Local Similarity 100.0%; Pred. NO. 0;

ALIGNMENTS

RESULT 1

US-08-121-713D-53
; Sequence 53, Application US/08121713D
; Patent No. 5639856
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey S.
; APPLICANT: Kolodkin, Alex L.
; APPLICANT: Matthes, David
; APPLICANT: Bentley, David R.
; APPLICANT: O'Connor, Timothy
; TITLE OF INVENTION: The Semaphorin Gene Family
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 Bush Street, Suite 3200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/121,713D
; FILING DATE: 13-SEP-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B94-002-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; TELEX:
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2601 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 16..2331
; US-08-121-713D-53

28	58.4	2.2	3560	2	US-09-060-692-59	Sequence 59, Appl
29	58.4	2.2	3560	3	US-08-833-391-59	Sequence 59, Appl
30	58.4	2.2	3560	4	US-09-060-610-59	Sequence 59, Appl
31	58.4	2.2	3560	5	PCT-US94-10151A-59	Sequence 59, Appl
32	55.6	2.1	4286	4	US-09-976-594-632	Sequence 632, App
33	54.8	2.0	2504	1	US-08-121-713D-63	Sequence 63, Appl
34	54.8	2.0	2504	1	US-08-835-268-63	Sequence 63, Appl
35	54.8	2.0	2504	2	US-09-060-692-63	Sequence 63, Appl
36	54.8	2.0	2504	3	US-08-833-391-63	Sequence 63, Appl
37	54.8	2.0	2504	4	US-09-060-610-63	Sequence 63, Appl
38	54.8	2.0	2504	5	PCT-US94-10151A-63	Sequence 63, Appl
39	54.6	2.0	2787	4	US-09-254-594-2	Sequence 2, Appl
40	54.6	2.0	3195	4	US-09-254-594-1	Sequence 1, Appl
41	48.6	1.8	2670	1	US-08-121-713D-61	Sequence 61, Appl
42	48.6	1.8	2670	1	US-08-835-268-61	Sequence 61, Appl
43	48.6	1.8	2670	2	US-09-060-692-61	Sequence 61, Appl
44	48.6	1.8	2670	3	US-08-833-391-61	Sequence 61, Appl
45	48.6	1.8	2670	4	US-09-060-610-61	Sequence 61, Appl

Matches 2509; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
Qy	193	CTGCAGCATGGGCTGTTAACTAGGATGCTGTCTTTCTTGGGAGATTAATCTACAGC	252
Dd	9	CTGCAGCATGGGCTGTTAACTAGGATGCTGTCTTTCTTGGGAGATTAATCTACAGC	68
Qy	253	AAAGAGCAAACTATCAGATGGGAAGAAACAATGTGCCAAGGCTGAATATCTCAACAAGA	312
Dd	69	AAAGAGCAAACTATCAGATGGGAAGAAACAATGTGCCAAGGCTGAATATCTCAACAAGA	128
Qy	313	AATGTTGGAAATCCAAATGTGATCACTTTCAATGGCTTGGCCAAACAGCTCCAGTTATCA	372
Dd	129	AATGTTGGAAATCCAAATGTGATCACTTTCAATGGCTTGGCCAAACAGCTCCAGTTATCA	188
Qy	373	TACCTTCCTTTTGGATGAGGAACGGAGTAGGCTGTATGTTGGAGCAAAAGGATCACATAT	432
Dd	189	TACCTTCCTTTTGGATGAGGAACGGAGTAGGCTGTATGTTGGAGCAAAAGGATCACATAT	248
Qy	433	TTCAATTCGACCTGGTTAAATCAAGATTTTCAAAAGATTTGTGGCCAGATCTTACAC	492
Dd	249	TTCAATTCGACCTGGTTAAATCAAGATTTTCAAAAGATTTGTGGCCAGATCTTACAC	308
Qy	493	CAGAAGAGATGAATCAAGTGGGCTGGAAAGACATCTGAAAGAAATGTGCTAATTTTCA	552
Dd	309	CAGAAGAGATGAATCAAGTGGGCTGGAAAGACATCTGAAAGAAATGTGCTAATTTTCA	368
Qy	553	CAAGGTACTTAAGGCATTAATCAGACTCATTGTGACGCTGTGGAACGGGGCTTTTCA	612
Dd	369	CAAGGTACTTAAGGCATTAATCAGACTCATTGTGACGCTGTGGAACGGGGCTTTTCA	428
Qy	613	TCCAAATTCACCTCAATTTGAATTTGGACATCATCTGAGGACATATTTTAAAGCTGGA	672
Dd	429	TCCAAATTCACCTCAATTTGAATTTGGACATCATCTGAGGACATATTTTAAAGCTGGA	488
Qy	673	GAACTCACATTTTGAATAACGGGCTGGGAAGTCCATATGACCTCAAGCTGTGACAGC	732
Dd	489	GAACTCACATTTTGAATAACGGGCTGGGAAGTCCATATGACCTCAAGCTGTGACAGC	548
Qy	733	ATCCCTTTTAAATAGATGGAGATTAATCTCGGAAGTCCAGCTGATTTATGGGGCGAGA	792
Dd	549	ATCCCTTTTAAATAGATGGAGATTAATCTCGGAAGTCCAGCTGATTTATGGGGCGAGA	608
Qy	793	CTTTGCTATCTTCGGAATCTTTGGGACACACCCCAATCAGGACAGGACGATGATTC	852
Dd	609	CTTTGCTATCTTCGGAATCTTTGGGACACACCCCAATCAGGACAGGACGATGATTC	668
Qy	853	CAGGTGGCTCAATGATCCAAAGTTCATTTAGTGGCCACCTCATCTCAGAGAGTGACATCC	912
Dd	669	CAGGTGGCTCAATGATCCAAAGTTCATTTAGTGGCCACCTCATCTCAGAGAGTGACATCC	728
Qy	913	TGAAGATGACAAAGTATATCTTTTCTCCGTGAAATGCAATAGATGGAGAACCTCTGG	972
Dd	729	TGAAGATGACAAAGTATATCTTTTCTCCGTGAAATGCAATAGATGGAGAACCTCTGG	788
Qy	973	AAAAGTACTCAGCTAGATAGGTTCAGATATGCAAGATGACATTTTGGAGGACAGAA	1032
Dd	789	AAAAGTACTCAGCTAGATAGGTTCAGATATGCAAGATGACATTTTGGAGGACAGAA	848
Qy	1033	TTGTGTAATAATGGACAAATCTCTCAAAGCTGCTGATTTGCTCAGTGGCAGGTCC	1092
Dd	849	TTGTGTAATAATGGACAAATCTCTCAAAGCTGCTGATTTGCTCAGTGGCAGGTCC	908
Qy	1093	AAATGGCATTTGACACTCAATTTTGAATGAACTGACAGATGATTTCTTAATGAATTAAGA	1152
Dd	909	AAATGGCATTTGACACTCAATTTTGAATGAACTGACAGATGATTTCTTAATGAATTAAGA	968
Qy	1153	TCTTAAATTCAGTTGATATGAGAGTGTTCAGACTTCCAGTAAACATTTTCAAGGATC	1212
Dd	969	TCTTAAATTCAGTTGATATGAGAGTGTTCAGACTTCCAGTAAACATTTTCAAGGATC	1028
Qy	1213	AGCCGTGTGTATGATGATGAGTGTGAGAGGAGTGTTCCTTGTGCTCATATGCCCA	1272
Dd	1029	AGCCGTGTGTATGATGATGAGTGTGAGAGGAGTGTTCCTTGTGCTCATATGCCCA	1088

Qy	1273	CAGGATGGACCCCAACTATCAATGGTGGCTTATCAAGGAAGAGTCCCTTATCAAGGCC	1332
Dd	1089	CAGGATGGACCCCAACTATCAATGGTGGCTTATCAAGGAAGAGTCCCTTATCAAGGCC	1148
Qy	1333	AGGAACTTGTCTCCAGCAAAACATTTGGTGGTGTGACTCTACAAAGGACCTTCTCTGATGA	1392
Dd	1149	AGGAACTTGTCTCCAGCAAAACATTTGGTGGTGTGACTCTACAAAGGACCTTCTCTGATGA	1208
Qy	1393	TGTTATACCTTTGCAAGAAGTCTATCCAGCATGTACAAATCCAGTGTTCCTATGAACAA	1452
Dd	1209	TGTTATACCTTTGCAAGAAGTCTATCCAGCATGTACAAATCCAGTGTTCCTATGAACAA	1268
Qy	1453	TGCCCCAATAGTGTATCAAAACGGGATGTAAATTTTCAATTTTACACAAATTTCTGTAGACCG	1512
Dd	1269	TGCCCCAATAGTGTATCAAAACGGGATGTAAATTTTCAATTTTACACAAATTTCTGTAGACCG	1328
Qy	1513	AGTGAATCAGAAAGATGGAAGATGATGTATGTATTTATCGGAACAGATTTCTGGACCGT	1572
Dd	1329	AGTGAATCAGAAAGATGGAAGATGATGTATGTATTTATCGGAACAGATTTCTGGACCGT	1388
Qy	1573	TCCTTAAAGTGTGTTCAATTCCTAAGGAGACTTGGTATGATTTTAGAAGAGGTTCTGTGGA	1632
Dd	1389	TCCTTAAAGTGTGTTCAATTCCTAAGGAGACTTGGTATGATTTTAGAAGAGGTTCTGTGGA	1448
Qy	1633	AGAAATGACAGTGTTCCTGGGAACCGACTGTATTTAGCAATAGGAGCTTCTCAATAGCA	1692
Dd	1449	AGAAATGACAGTGTTCCTGGGAACCGACTGTATTTAGCAATAGGAGCTTCTCAATAGCA	1508
Qy	1693	GCAACAACTATATATTTGGTTTCAACGGCTGGGGTTGCCAGCTCCCTTTACACCGGTGTGA	1752
Dd	1509	GCAACAACTATATATTTGGTTTCAACGGCTGGGGTTGCCAGCTCCCTTTACACCGGTGTGA	1568
Qy	1753	TATTTACGGGAACAGGTGTGCTGATGTGCTGCTGCCCGGAGACCTTCTACCTGTCTGGGA	1812
Dd	1569	TATTTACGGGAACAGGTGTGCTGATGTGCTGCTGCCCGGAGACCTTCTACCTGTCTGGGA	1628
Qy	1813	TGGTTCTCATGTTCTCGCTATTTTCCCACTGCAAAAGAGACGCAAGACGCAAGATAT	1872
Dd	1629	TGGTTCTCATGTTCTCGCTATTTTCCCACTGCAAAAGAGACGCAAGACGCAAGATAT	1688
Qy	1873	AGAAATGGAGACCCACTGACTCTCTGTTAGAGTATACCATGATTAATCAGATGGCCA	1932
Dd	1689	AGAAATGGAGACCCACTGACTCTCTGTTAGAGTATACCATGATTAATCAGATGGCCA	1748
Qy	1933	CAGCCCTGAAGAGAGATCATCTATGTTAGAGATAGTAGACATTTTGGAAATGCGAG	1992
Dd	1749	CAGCCCTGAAGAGAGATCATCTATGTTAGAGATAGTAGACATTTTGGAAATGCGAG	1808
Qy	1993	TCCGAAGTCCGAGAGAGGCTGTGTTATTTGGCAATTTCCAGAGCGGAATTAAGAGCGAAA	2052
Dd	1809	TCCGAAGTCCGAGAGAGGCTGTGTTATTTGGCAATTTCCAGAGCGGAATTAAGAGCGAAA	1868
Qy	2053	AGAGAGATCAGAGTGGATGATATATCATCAGACAGATCAAGGCTTCTGTGATGCTAG	2112
Dd	1869	AGAGAGATCAGAGTGGATGATATATCATCAGACAGATCAAGGCTTCTGTGATGCTAG	1928
Qy	2113	TCTCAACAGAGAGATTCAGGCAATTTACCTCTGCGCATGGGTGGACATGGGTTCATACA	2172
Dd	1929	TCTCAACAGAGAGATTCAGGCAATTTACCTCTGCGCATGGGTGGACATGGGTTCATACA	1988
Qy	2173	AATCTTCTTAAAGTAAACCTTGGGAAGTCAATTGACACAGAGATTTGGAAAGACTTCTTCA	2232
Dd	1989	AATCTTCTTAAAGTAAACCTTGGGAAGTCAATTGACACAGAGATTTGGAAAGACTTCTTCA	2048
Qy	2233	TAAAGATGATGATGGAGATGGCTTAAAGCAAAAGAAATGTCCATAGATGACATGACCTAG	2292
Dd	2049	TAAAGATGATGATGGAGATGGCTTAAAGCAAAAGAAATGTCCATAGATGACATGACCTAG	2108
Qy	2293	CCAGAGGTCTGGTACAGAGACTTTCATGAGCTCATCAACCCACCCCAATCTCAACAGCAT	2352
Dd	2109	CCAGAGGTCTGGTACAGAGACTTTCATGAGCTCATCAACCCACCCCAATCTCAACAGCAT	2168

Db 969 TCCTAAAAATCCAGTTGTATATGAGAGTGTTCAGACTTCCAGTACATTTTCAAGGGATC 1028
Qy 1213 AGCCGTGTATGTATAGATGAGTGAAGAGGAGTGTTCCTTGGTCCATATGCCA 1272
Db 1029 AGCCGTGTATGTATAGATGAGTGAAGAGGAGTGTTCCTTGGTCCATATGCCA 1088
Qy 1273 CAGGGATGGAACCAACTATCAATGGGTGCTTTATCAAGGAAGAGTCCCTTATCCACGCCC 1332
Db 1089 CAGGGATGGAACCAACTATCAATGGGTGCTTTATCAAGGAAGAGTCCCTTATCCACGCCC 1148
Qy 1333 AGGAATGTCGACAGACCAATGTTGGTGTTCGACTCTCAAGAGGACCTTCCTGATGA 1392
Db 1149 AGGAATGTCGACAGACCAATGTTGGTGTTCGACTCTCAAGAGGACCTTCCTGATGA 1208
Qy 1393 TGTATTAACCTTTGCAAGAGTCAATCCAGCCATGTACAATCCAGTGTTCCTATGAACAA 1452
Db 1209 TGTATTAACCTTTGCAAGAGTCAATCCAGCCATGTACAATCCAGTGTTCCTATGAACAA 1268
Qy 1453 TCGCCCAATAGTATCAAAACCGATGTAAATTTATCAATTTACAAATTTGCTAGACCG 1512
Db 1269 TCGCCCAATAGTATCAAAACCGATGTAAATTTATCAATTTACAAATTTGCTAGACCG 1328
Qy 1513 AGTGGATGCAAGATGAGCAGTATGATGTATGTTTATCGGAACAGATGTTGGACCGT 1572
Db 1329 AGTGGATGCAAGATGAGCAGTATGATGTATGTTTATCGGAACAGATGTTGGACCGT 1388
Qy 1573 TCTTAAAGTAGTTCATTTCCCTAAGGAGCTGTTGATGATTTAGAGAGTTCCTGCGGA 1632
Db 1389 TCTTAAAGTAGTTCATTTCCCTAAGGAGCTGTTGATGATTTAGAGAGTTCCTGCGGA 1448
Qy 1633 AGAATGACAGTTCCTCGGGAACCGACTCTATTTTCAGCAATGGAGCTTTCCCAATAGCA 1692
Db 1449 AGAATGACAGTTCCTCGGGAACCGACTCTATTTTCAGCAATGGAGCTTTCCCAATAGCA 1508
Qy 1693 GCACAACTATATTTGTTTCAACCGCTGGGTTGCCAGCTCCCTTTACACCGGTGGA 1752
Db 1509 GCACAACTATATTTGTTTCAACCGCTGGGTTGCCAGCTCCCTTTACACCGGTGGA 1568
Qy 1753 TATTTACGGAAGAGCGTGTCTGAGTGTTCCTCGCCGAGACCTTACTGTGTTGGGA 1812
Db 1569 TATTTACGGAAGAGCGTGTCTGAGTGTTCCTCGCCGAGACCTTACTGTGTTGGGA 1628
Qy 1813 TGGTTCGATGTTCTCGCTATTTTCCCACTGCAAGAGAGCGCACAGACAGATAT 1872
Db 1629 TGGTTCGATGTTCTCGCTATTTTCCCACTGCAAGAGAGCGCACAGACAGATAT 1688
Qy 1873 AAGAAATGGAGACCCACTGACTCACTGTTTCAGACTTACACCATGATATCACCATGGCCA 1932
Db 1689 AAGAAATGGAGACCCACTGACTCACTGTTTCAGACTTACACCATGATATCACCATGGCCA 1748
Qy 1933 CAGCCCTGAAGAGAGATCATCTATGTTGAGAGATAGTAGCAGTTCCTTGGATGCGAG 1992
Db 1749 CAGCCCTGAAGAGAGATCATCTATGTTGAGAGATAGTAGCAGTTCCTTGGATGCGAG 1808
Qy 1993 TCCGAAGTCGACAGAGCGCTGCTTATTTGGCAATTTCCAGAGGCGGAAATGAAGAGCGAAA 2052
Db 1809 TCCGAAGTCGACAGAGCGCTGCTTATTTGGCAATTTCCAGAGGCGGAAATGAAGAGCGAAA 1868
Qy 2053 AGAAGAGTCAGAGTGGATGATCATCATCAGGACAGATCAAGGCTTCCTGCTAGTAG 2112
Db 1869 AGAAGAGTCAGAGTGGATGATCATCATCAGGACAGATCAAGGCTTCCTGCTAGTAG 1928
Qy 2113 TCTACAAAGAGAGTTCAGGCAATTTACTCTGCTGATCGGTTGGAACATGGGTTTATACA 2172
Db 1929 TCTACAAAGAGAGTTCAGGCAATTTACTCTGCTGATCGGTTGGAACATGGGTTTATACA 1988
Qy 2173 ACTCTCTTAAAGTAACTCGGAGTCAATTCACACAGAGCATTTGGAGAGCTTCCTTCA 2232
Db 1989 ACTCTCTTAAAGTAACTCGGAGTCAATTCACACAGAGCATTTGGAGAGCTTCCTTCA 2048
Qy 2233 TAAAGATGATGAGAGTGGCTCTTAAGACCAAGAAATGTCCCAATAGCATGACACTAG 2292
Db 2049 TAAAGATGATGAGAGTGGCTCTTAAGACCAAGAAATGTCCCAATAGCATGACACTAG 2108

Qy 2293 CCAGAAGCTCTGGTACAGAGACTTTCATGAGCTCATCAACCCCAATCTCAACACGAT 2352
Db 2109 CCAGAAGCTCTGGTACAGAGACTTTCATGAGCTCATCAACCCCAATCTCAACACGAT 2168
Qy 2353 GGATGAGTCTGTGTGAACAGTTCGAAAAGGGACCCGAAAACAACTGCGGCAAGGCGAGG 2412
Db 2169 GGATGAGTCTGTGTGAACAGTTCGAAAAGGGACCCGAAAACAACTGCGGCAAGGCGAGG 2228
Qy 2413 ACATACCCCGGACAGTACAAATGGAAGCACTTACAGAGAAATAAGAAAGGTAGAAA 2472
Db 2229 ACATACCCCGGACAGTACAAATGGAAGCACTTACAGAGAAATAAGAAAGGTAGAAA 2288
Qy 2473 CAGGAGGACCCCAAAATTTGAGAGGGACCCGAGAGTGTCTGAGCTGCATCTCTAGA 2532
Db 2289 CAGGAGGACCCCAAAATTTGAGAGGGACCCGAGAGTGTCTGAGCTGCATCTCTAGA 2348
Qy 2533 AACCTCAACCAAGTAGAAGTTCGCTAGACAAATACTGGAAAAACAAATGCTATATACAT 2592
Db 2349 AACCTCAACCAAGTAGAAGTTCGCTAGACAAATACTGGAAAAACAAATGCTATATACAT 2408
Qy 2593 GAACCTTTTTCATGGCAATATGAGATGTTTACAATGGTGGGAAATTCAGCTGAGTTCCA 2652
Db 2409 GAACCTTTTTCATGGCAATATGAGATGTTTACAATGGTGGGAAATTCAGCTGAGTTCCA 2468
Qy 2653 CCAATTATAAATTAATCCATGAGTAACTTTCCTTAATAGGCTTTTTCCTC 2702
Db 2469 CCAATTATAAATTAATCCATGAGTAACTTTCCTTAATAGGCTTTTTCCTC 2518

RESULT 3

US-09-060-692-53
; Sequence 53, Application US/09060692
; Patent No. 5935865
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey S.
; APPLICANT: Koldokin, Alex L.
; APPLICANT: Matthes, David
; APPLICANT: Bentley, David R.
; APPLICANT: O'Connor, Timothy
; TITLE OF INVENTION: The Semaphorin Gene Family
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 Bush Street, Suite 3200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/060,692
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/121,713
; FILING DATE: 13-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B94-002-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; TELEX:
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2601 base pairs
; TYPE: nucleic acid

STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cdna
FEATURE:
NAME/KEY: CDS
LOCATION: 16..2331
US-09-060-692-53

Query Match 92.6%; Score 2508.4; DB 2; Length 2601;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2509; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	193	CTG CAG CAT GGG GTG TTA CTA C T A G G A T T G T C T G T T T C T G G G A G A T T A C T T A C A G C	252
DB	9	CTG CAG CAT GGG GTG TTA CTA C T A G G A T T G T C T G T T T C T G G G A G A T T A C T T A C A G C	68
QY	253	A G A G C A A A C T A T C A G A A T G G G A G A A C A A T G T G C C A A G G C T G A A A T T A C C T C A A A G A	312
DB	69	A A G A G C A A A C T A T C A G A A T G G G A G A A C A A T G T G C C A A G G C T G A A A T T A C C T C A A A G A	128
QY	313	A A T G T T G G A A T C C A A C A A T G T A T C A C T T T C A A T G S C T T G G C C A A C A G C T C C A G T T A T C A	372
DB	129	A A T G T T G G A A T C C A A C A A T G T A T C A C T T T C A A T G S C T T G G C C A A C A G C T C C A G T T A T C A	188
QY	373	T A C C T T C C T T T G G A T G A G A A C G G A T A G G C T G T A T G T T G A G C A A A G A A T C A C A T A T T	432
DB	189	T A C C T T C C T T T G G A T G A G A A C G G A T A G G C T G T A T G T T G A G C A A A G A A T C A C A T A T T	248
QY	433	T T C A T T C G A C C T G G T T A A T A T C A A G A T T T C A A A G A T T G T G C C A G T A T C T T A C A C	492
DB	249	T T C A T T C G A C C T G G T T A A T A T C A A G A T T T C A A A G A T T G T G C C A G T A T C T T A C A C	308
QY	493	C A G A G A G A T G A A T G C A A G T G G C T G G A A A G A C A C A T C T G A A G A T G T G T A A T T T C A T	552
DB	309	C A G A G A G A T G A A T G C A A G T G G C T G G A A A G A C A C A T C T G A A G A T G T G T A A T T T C A T	368
QY	553	C A A G T A C T T A A G G C A T A P A A T C A G A C T C A C T T G A C G C T T G G A A C G G G G C T T T T C A	612
DB	369	C A A G T A C T T A A G G C A T A P A A T C A G A C T C A C T T G A C G C T T G G A A C G G G G C T T T T C A	428
QY	613	T C C A A T T T G C A C T C A T G A A T T T G G A C A T C A T C C T G A G A C A N A T T T T T A A G C T G G A	672
DB	429	T C C A A T T T G C A C T C A T G A A T T T G G A C A T C A T C C T G A G A C A N A T T T T T A A G C T G G A	488
QY	673	G A A C T C A C A T T T G A A A A C G G C G T G G A A G A G T C C A T A T G A C C C T A A G C T G C T G A C A G C	732
DB	489	G A A C T C A C A T T T G A A A A C G G C G T G G A A G A G T C C A T A T G A C C C T A A G C T G C T G A C A G C	548
QY	733	A T C C C T T T T A T A G A T G A G A A T T A C T C T G G A A C T C A G C T G A T T T T A T G G G C G A G A	792
DB	549	A T C C C T T T T A T A G A T G A G A A T T A C T C T G G A A C T C A G C T G A T T T T A T G G G C G A G A	608
QY	793	C T T T G C T A T C T T C C G A A C T T T G G C A C C A C C A C C A T C A G G A C A G A G A G A T T C	852
DB	609	C T T T G C T A T C T T C C G A A C T T T G G C A C C A C C A C C A T C A G G A C A G A G A G A T T C	668
QY	853	C A G G T G G C T C A A T G A T C A A A G T T C A A T T A G T G C C C A C C T C A T C T C A G A G A T G A C A A T C C	912
DB	669	C A G G T G G C T C A A T G A T C A A A G T T C A A T T A G T G C C C A C C T C A T C T C A G A G A T G A C A A T C C	728
QY	913	T G A G A T C A C A A A G T A T A C T T T T C C G T G A A A T G C A A T A G A T A G A G A A C A C T C T G G	972
DB	729	T G A G A T C A C A A A G T A T A C T T T T C C G T G A A A T G C A A T A G A T A G A G A A C A C T C T G G	788
QY	973	A A A A G C T A C T C A C G C T A G A T A G T C A G A T A T G C A A G A A T G A C T T T T G A G G G C A C A G A G	1032
DB	789	A A A A G C T A C T C A C G C T A G A T A G T C A G A T A T G C A A G A A T G A C T T T T G A G G G C A C A G A G	848
QY	1033	T C T G T G A A T A A A T G G A C A A C A T T C C T C A A A G C T C G T C T G A T T T G C T C A G T G C A G G T C C	1092
DB	849	T C T G T G A A T A A A T G G A C A A C A T T C C T C A A A G C T C G T C T G A T T T G C T C A G T G C A G G T C C	908
QY	1093	A A A T G G C A T T G A C A C T C A T T T T G A T G A A C T C A G G A T G A T T C C T A T A T G A C T T T A A A G A	1152

DB	909	A A A T G G C A T T G A C A C T C A T T T T G A T G A A C T C A G A A T G T A T T C C T A T A T G A C T T T A A A G A	968
QY	1153	T C C T A A A A A T C C A G T T G T A T A T G A G A T G T T T A C G A C T T C C A G T A A C A T T T T C A A G G G A T C	1212
DB	969	T C C T A A A A A T C C A G T T G T A T A T G A G A T G T T T A C G A C T T C C A G T A A C A T T T T C A A G G G A T C	1028
QY	1213	A G C C G T G T A T G T A T A T A C A T C A G T A T G T C A G A A G G G T T C C T T G T G C C A T A T G C C C A	1272
DB	1029	A G C C G T G T A T G T A T A T A C A T C A G T A T G T G A A A G G G T T C C T T G T G C C A T A T G C C C A	1088
QY	1273	C A G G A T G G A C C C A A C T A T C A A T G G T G C C T T A T C A A G A A G A G T C C C C T A T C C A C G G C C	1332
DB	1089	C A G G A T G G A C C C A A C T A T C A A T G G T G C C T T A T C A A G A A G A G T C C C C T A T C C A C G G C C	1148
QY	1333	A G G A A C T T G T C C C A G A C A A A C A T T T G T G T T T G A C T C T A C A A A G A C A C T T T C C T G A T G A	1392
DB	1149	A G G A A C T T G T C C C A G A C A A A C A T T T G T G T T T T G A C T C T A C A A A G A C A C T T T C C T G A T G A	1208
QY	1393	T G T T A T A A C C T T T C A A A A G A T C A T C C A G C C A T G A C A A T C C A G T G T T T C C T A T A A C A A	1452
DB	1209	T G T T A T A A C C T T T C A A A A G A T C A T C C A G C C A T G A C A A T C C A G T G T T T C C T A T A A C A A	1268
QY	1453	T C G C C C A A T A G T A T C A A A C G G A T G T A A A T T A T C A A T T T A C A A A A T T G T C G T A G A C C G	1512
DB	1269	T C G C C C A A T A G T A T C A A A C G G A T G T A A A T T A T C A A T T T A C A A A A T T G T C G T A G A C C G	1328
QY	1513	A G T G G A T C C A A A G A T G G A C A G A T G A T G T A T G T T T A T C G G A A C A G A T G T T G G A C C G T	1572
DB	1329	A G T G G A T C C A A A G A T G G A C A G A T G A T G T A T G T T T A T C G G A A C A G A T G T T G G A C C G T	1388
QY	1573	T C T T A A A G T A G T T T C A A T T C C T A A G A G A C T T G G T A T G A T T A G A A G A G T T C T G T G G A	1632
DB	1389	T C T T A A A G T A G T T T C A A T T C C T A A G A G A C T T G G T A T G A T T A G A A G A G T T C T G T G G A	1448
QY	1633	A G A A T C A C A G A T T T T T C G G A A C C G A C T G A T T A T G T T T A T C G G A A C A G A T G T T C C A T A G C A	1692
DB	1449	A G A A T C A C A G A T T T T T C G G A A C C G A C T G A T T A T G T T T A T C G G A A C A G A T G T T C C A T A G C A	1508
QY	1693	G C A A C A C T A T A T A T T G G T T C A A C G G C T G G G G T G C C C A G C T C C C T T T A C A C C G G T G T G A	1752
DB	1509	G C A A C A C T A T A T A T T G G T T C A A C G G C T G G G G T G C C C A G C T C C C T T T A C A C C G G T G T G A	1568
QY	1753	T A T T A T G G G A A A G C G T G C T G A G T G T T G C C T C G C C C G A G A C C C T A C T G T G C T T G G G A	1812
DB	1569	T A T T A T G G G A A A G C G T G C T G A G T G T T G C C T C G C C C G A G A C C C T A C T G T G C T T G G G A	1628
QY	1813	T G G T T C T G C A T G T T C T C G C T A T T T T C C C A C T G C A A A G A G A C G C A A G A C G A C A A G A T A T	1872
DB	1629	T G G T T C T G C A T G T T C T C G C T A T T T T C C C A C T G C A A A G A G A C G C A A G A C G A C A A G A T A T	1688
QY	1873	A A G A A T G G A G A C C C A C T G A C T C A C T G T T C A G A C T T A C A C C A T G A T A A T C A C C A T G G C C A	1932
DB	1689	A A G A A T G G A G A C C C A C T G A C T C A C T G T T C A G A C T T A C A C C A T G A T A A T C A C C A T G G C C A	1748
QY	1933	C A C C C T G A A G A G A G A A T C A T C T A T G T G T G A G A A T A G T A G C A C A T T T T T C G A A T G C A G	1992
DB	1749	C A C C C T G A A G A G A G A A T C A T C T A T G T G T A G A A A T A G T A G C A C A T T T T T G G A A T G C A G	1808
QY	1993	T C C A A G T C C G A G A G A G C C T G G T C T A T T T G C A A T T C C A G A G C G A A A T A A A G A G C G A A A	2052
DB	1809	T C C A A G T C C G A G A G A G C C T G G T C T A T T T G C A A T T C C A G A G C G A A A T A A A G A G C G A A A	1868
QY	2053	A G A A G A G A T C A G A T G A T C A T A T C A T C A G G A C A G A T C A A G C C T T C T G C T A G T A G	2112
DB	1869	A G A A G A G A T C A G A T G A T C A T A T C A T C A G G A C A G A T C A A G C C T T C T G C T A G T A G	1928
QY	2113	T C T A C A A G A A A G A G T T C A G G C A A T T A C C T C T G C C A T G C G G T G G A A C A T G G G T T C A T A C A	2172
DB	1929	T C T A C A A G A A A G A G T T C A G G C A A T T A C C T C T G C C A T G C G G T G G A A C A T G G G T T C A T A C A	1988
QY	2173	A A C T C T T C T T A A G G T A A C C C T G G A A G T C A T T G A C A C A G A C A T T T G G A A G A A C T T C T T C A	2232

Db 1989 AACTCTCTTAAGGTAACCCCTGGAGTCATGACACAGAGCAATTTGGAAAGAACTCTTCA 2048
QY 2233 TAAAGATGATGATGAGATGGCTCTAAGACCAAGAAATGTCCAATAGCATGACACCTAG 2292
Db 2049 TAAAGATGATGATGAGATGGCTCTAAGACCAAGAAATGTCCAATAGCATGACACCTAG 2108
QY 2293 CCAGAAGTCTGTGTACAGAGACTTCATGAGCTCATCAACCCACCCCACTCTCAACAGAT 2352
Db 2109 CCAGAGGTCTGTGTACAGAGACTTCATGAGCTCATCAACCCACCCCACTCTCAACAGAT 2188
QY 2353 GGATGAGTCTGTGTACAGAGACTTCATGAGCTCATCAACCCACCCCACTCTCAACAGAT 2412
Db 2169 GGATGAGTCTGTGTACAGAGACTTCATGAGCTCATCAACCCACCCCACTCTCAACAGAT 2228
QY 2413 ACATACCCCGGGAACAGTACAAATGGAGCACTTACAGAAATAGAAAGGTAGAAA 2472
Db 2229 ACATACCCCGGGAACAGTACAAATGGAGCACTTACAGAAATAGAAAGGTAGAAA 2288
QY 2473 CAGAGGACCCAGAAATTTGAGAGGACCCAGAGTGTCTGAGTGCATTACCTCTAGA 2532
Db 2289 CAGAGGACCCAGAAATTTGAGAGGACCCAGAGTGTCTGAGTGCATTACCTCTAGA 2348
QY 2533 AACCTCAAAAGTAGAAAATTCGCTAGACAATACTGGAAACAAATGCAATATACAT 2592
Db 2349 AACCTCAAAAGTAGAAAATTCGCTAGACAATACTGGAAACAAATGCAATATACAT 2408
QY 2593 GAACCTTTTTCATGGCAATTTGAGATGTTTCAATGTTGAGGAAATTCAGTGTGCTCA 2652
Db 2409 GAACCTTTTTCATGGCAATTTGAGATGTTTCAATGTTGAGGAAATTCAGTGTGCTCA 2468
QY 2653 CCAATTATAAATTAATCCATGAGTAACTTTCCTATAGCTTTTTC 2702
Db 2469 CCAATTATAAATTAATCCATGAGTAACTTTCCTATAGCTTTTTC 2518

RESULT 4

US-08-833-391-53
; Sequence 53, Application US/08833391
; Patent No. 6013781
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey S.
; APPLICANT: Kolodkin, Alex L.
; APPLICANT: Matches, David
; APPLICANT: Bentley, David R.
; APPLICANT: O'Connor, Timothy
; TITLE OF INVENTION: The Semaphorin Gene Family
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 Bush Street, Suite 3200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833,391
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/121,713
; FILING DATE: 13-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B94-002-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)343-4341
; TELEFAX: (415) 343-4342

TELEX:
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2601 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 16...2331
; US-08-833-391-53

Query Match 92.6%; Score 2508.4; DB 3; Length 2601;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2509; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 193 CTGCAGCATGGGCTGGTTAACTAGGATGTCTCTTTCTGGGAGATTAATTACACG 252
Db 9 CTGCAGCATGGGCTGGTTAACTAGGATGTCTCTTTCTGGGAGATTAATTACACG 68
QY 253 AAGACCAAACTATCAGAAATGGAAAGAAACAATGTGCCAAGGCTGAAATTTATCCCTACAAAGA 312
Db 69 AAGACCAAACTATCAGAAATGGAAAGAAACAATGTGCCAAGGCTGAAATTTATCCCTACAAAGA 128
QY 313 AATGTTGGAATCCAAATGTGATCACTTTCAATGGCTTGGCCAAACAGCTCCAGTTATCA 372
Db 129 AATGTTGGAATCCAAATGTGATCACTTTCAATGGCTTGGCCAAACAGCTCCAGTTATCA 188
QY 373 TACCTTCTCTTTGGATCAGGAACCGAGTAGGCTGTATGTTGGAGCAAGGATCACATATT 432
Db 189 TACCTTCTCTTTGGATCAGGAACCGAGTAGGCTGTATGTTGGAGCAAGGATCACATATT 248
QY 433 TTCAATCGACCTGGTTAATCAAGGATTTTCAAAAGATTGTGGCCAGTATCTTACAC 492
Db 249 TTCAATCGACCTGGTTAATCAAGGATTTTCAAAAGATTGTGGCCAGTATCTTACAC 308
QY 493 CAGAAGAGATGAATGCAAGTGGGCTGGAAAGACATCTTGAAGAAATGTCTTAATTTTCAAT 552
Db 309 CAGAAGAGATGAATGCAAGTGGGCTGGAAAGACATCTTGAAGAAATGTCTTAATTTTCAAT 368
QY 553 CAGGTACTTAAGCATATAATCAGACTCACTTTGAGGCTGTGGAAACGGGGCTTTTCA 612
Db 369 CAGGTACTTAAGCATATAATCAGACTCACTTTGAGGCTGTGGAAACGGGGCTTTTCA 428
QY 613 TCCAAATTTGACCTACATTTGAAATTTGACATCATCTGAGGACAAATATTTTAAAGCTGA 672
Db 429 TCCAAATTTGACCTACATTTGAAATTTGACATCATCTGAGGACAAATATTTTAAAGCTGA 488
QY 673 GAATCAGATTTGAAACGGGCTGGAGAGTCCATATGACCTTAAGCTCTGACAGC 732
Db 489 GAATCAGATTTGAAACGGGCTGGAGAGTCCATATGACCTTAAGCTCTGACAGC 548
QY 733 ATCCCTTTTATAGATGGAGAAATTTACTCTGGAATTCAGAGTGAATTTTATGGGCGAGA 792
Db 549 ATCCCTTTTATAGATGGAGAAATTTACTCTGGAATTCAGAGTGAATTTTATGGGCGAGA 608
QY 793 CTTTGTCTATCTTCGAACTCTGGGACCAACCAATCAGGACAGCAGCATGATTC 852
Db 609 CTTTGTCTATCTTCGAACTCTGGGACCAACCAATCAGGACAGCAGCATGATTC 668
QY 853 CAGTGGCTCAATGATCCAAAGTTCAATAGTGGCCACCTCATCTCAGAGAGTGACAATCC 912
Db 669 CAGTGGCTCAATGATCCAAAGTTCAATAGTGGCCACCTCATCTCAGAGAGTGACAATCC 728
QY 913 TGAAGATGACAAAGTATACATTTTCTCGTGAATGCAATAGATGGAGAACCTCTGG 972
Db 729 TGAAGATGACAAAGTATACATTTTCTCGTGAATGCAATAGATGGAGAACCTCTGG 788
QY 973 AAAAGCTACTCAGCTAGATAGGTGATGATATGCAAGAAATGACTTTGGAGGGGACAGAG 1032
Db 789 AAAAGCTACTCAGCTAGATAGGTGATGATATGCAAGAAATGACTTTGGAGGGGACAGAG 848

REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: B94-002-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
TELEX:
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 2601 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 16..2331
US-09-060-610-53

Query Match 92.6%; Score 2508.4; DB 4; Length 2601;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2509; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	193	CTGAGCATGGGCTGTTAACTAGGATTCCTCTCTTTCTGGGAGATTACTTACAGC	252
DB	9	CTGAGCATGGGCTGTTAACTAGGATTCCTCTCTTTCTGGGAGATTACTTACAGC	68
QY	253	AAGAGCAACTATCAGATGGGAAGAACAACTGTGCCAAGGCTGAAATATCTTACAAGA	312
DB	69	AAGAGCAACTATCAGATGGGAAGAACAACTGTGCCAAGGCTGAAATATCTTACAAGA	128
QY	313	AATGTTGGAATCAACAATGTGATCACTTTCAATGGCTTGGCCACAGCTCCAGTTATCA	372
DB	129	AATGTTGGAATCAACAATGTGATCACTTTCAATGGCTTGGCCACAGCTCCAGTTATCA	188
QY	373	TACCTTCCCTTTGGATGAGGACGAGTAGGCTGTATGTGGAGCAGAGGATCATATT	432
DB	189	TACCTTCCCTTTGGATGAGGACGAGTAGGCTGTATGTGGAGCAGAGGATCATATT	248
QY	433	TTCAATGCACTGGTTAAATCAAGGATTTTCAAAAGATTTGTGGCCAGTATCTTACAC	492
DB	249	TTCAATGCACTGGTTAAATCAAGGATTTTCAAAAGATTTGTGGCCAGTATCTTACAC	308
QY	493	CAGAGAGATGATCAAGTGGGCTGGAAAGACATCTGAAAGATGTGCTAATTTTCAAT	552
DB	309	CAGAGAGATGATCAAGTGGGCTGGAAAGACATCTGAAAGATGTGCTAATTTTCAAT	368
QY	553	CAAGGTACTTAAGGCATATAATCAGACTCATCTGTACGCTGTGGAACGGGGCTTTTCA	612
DB	369	CAAGGTACTTAAGGCATATAATCAGACTCATCTGTACGCTGTGGAACGGGGCTTTTCA	428
QY	613	TCCAAATTTGACCTACATTTGAATTTGACATCATCTGAGGACATATTTTAAAGCTTGA	672
DB	429	TCCAAATTTGACCTACATTTGAATTTGACATCATCTGAGGACATATTTTAAAGCTTGA	488
QY	673	GAACTCACATTTTGAACCGGCTGGGAAGAGTCCATATGACCTAAGCTGTGACAGC	732
DB	489	GAACTCACATTTTGAACCGGCTGGGAAGAGTCCATATGACCTAAGCTGTGACAGC	548
QY	733	ATCCCTTTTAAATAGATGGAGAAATTAATCTGGAAGTCTGAGTATTTATGGGGCGAGA	792
DB	549	ATCCCTTTTAAATAGATGGAGAAATTAATCTGGAAGTCTGAGTATTTATGGGGCGAGA	608
QY	793	CTTTGCTATCTTCCGAATCTTTGGGACACACCAATCATGAGCAGAGCAGCATGATTC	852
DB	609	CTTTGCTATCTTCCGAATCTTTGGGACACACCAATCATGAGCAGAGCAGCATGATTC	668
QY	853	CAGTGGCTCAATGATCCAAAGTTTCAATAGTCCCACTCATCTCAGAGAGTGACATTC	912
DB	669	CAGTGGCTCAATGATCCAAAGTTTCAATAGTCCCACTCATCTCAGAGAGTGACATTC	728
QY	913	TGAAGATGACAAAGTATATCTTTTCTTCCGTGAAATGCAATAGATGAGAACACTCTGG	972
DB	729	TGAAGATGACAAAGTATATCTTTTCTTCCGTGAAATGCAATAGATGAGAACACTCTGG	788

QY	973	AAAAGCTACTCAGCTAGAAATAGCTCAGATATGCAAGAAATGACTTTGGAGGGCACAAGAAG	1032
DB	789	AAAAGCTACTCAGCTAGAAATAGCTCAGATATGCAAGAAATGACTTTGGAGGGCACAAGAAG	848
QY	1033	TCCTGTGAATAAATGGACAAATTCCTCAAGAGCTGCTGATTTGCTCAGTGCAGGTCC	1092
DB	849	TCCTGTGAATAAATGGACAAATTCCTCAAGAGCTGCTGATTTGCTCAGTGCAGGTCC	908
QY	1093	AAATGGCAATTCAGCTCATTTTGAATGAATGCAAGTGTATTCCTAATGAATTTTAAAGA	1152
DB	909	AAATGGCAATTCAGCTCATTTTGAATGAATGCAAGTGTATTCCTAATGAATTTTAAAGA	968
QY	1153	TCCTAAAAATCCAGTTGTATATGAGTGTTCAGACTTCCAGTAAATTTTCAAGGATC	1212
DB	969	TCCTAAAAATCCAGTTGTATATGAGTGTTCAGACTTCCAGTAAATTTTCAAGGATC	1028
QY	1213	AGCCGTGTATGTATAGCATGATGTGAGAAGGTGTTCCTTGGTCCATATGCCCA	1272
DB	1029	AGCCGTGTATGTATAGCATGATGTGAGAAGGTGTTCCTTGGTCCATATGCCCA	1088
QY	1273	CAGGATCGACCCAACTATCAATCGGTGCTTATCAAGGAAGAGTCCCTATCCAGGCC	1332
DB	1089	CAGGATCGACCCAACTATCAATCGGTGCTTATCAAGGAAGAGTCCCTATCCAGGCC	1148
QY	1333	AGGAATTTGTCCAGCAAAACATTTGGTGGTGTGACTCTACAAAGGACCTTCTCTGATGA	1392
DB	1149	AGGAATTTGTCCAGCAAAACATTTGGTGGTGTGACTCTACAAAGGACCTTCTCTGATGA	1208
QY	1393	TGTTATAACCTTTGCAAGAGTCAATCCAGCATGTACATCCAGTGTTCCTATGACAA	1452
DB	1209	TGTTATAACCTTTGCAAGAGTCAATCCAGCATGTACATCCAGTGTTCCTATGACAA	1268
QY	1453	TGCCCCAATAGTCAATCAAAACGAGTGTAAATATCAATTTACAAATTTCTGTAGACCG	1512
DB	1269	TGCCCCAATAGTCAATCAAAACGAGTGTAAATATCAATTTACAAATTTCTGTAGACCG	1328
QY	1513	AGTGAATCGCAAGATGGAACAGTATGATTTATTCGGAACAGATTTGGGACCGT	1572
DB	1329	AGTGAATCGCAAGATGGAACAGTATGATTTATTCGGAACAGATTTGGGACCGT	1388
QY	1573	TCCTTAACTAGTTCCTAATTCCTAAGGAGACTTGGTATGATTTAGAAAGAGTTCGTGGA	1632
DB	1389	TCCTTAACTAGTTCCTAATTCCTAAGGAGACTTGGTATGATTTAGAAAGAGTTCGTGGA	1448
QY	1633	AGAAATGACAGTTCCTGGGAAACCGACTGCTATTCAGCAATCGAGCTTCCACTAAGCA	1692
DB	1449	AGAAATGACAGTTCCTGGGAAACCGACTGCTATTCAGCAATCGAGCTTCCACTAAGCA	1508
QY	1693	GCAACAACTATATATTTGTTTCAACGGCTGGGGTTCGCCAGCTCCCTTTACACCGGTGGA	1752
DB	1509	GCAACAACTATATATTTGTTTCAACGGCTGGGGTTCGCCAGCTCCCTTTACACCGGTGGA	1568
QY	1753	TATTTACGGGAACCGTGTGCTGAGTTCGCTCGCCCGAGAGCCCTTACTGTGCTTGGGA	1812
DB	1569	TATTTACGGGAACCGTGTGCTGAGTTCGCTCGCCCGAGAGCCCTTACTGTGCTTGGGA	1628
QY	1813	TGTTCTCTCATGTTCTCGCTATTTTCCCACTGCAAAAGAGACGCAAGACGCAAGATAT	1872
DB	1629	TGTTCTCTCATGTTCTCGCTATTTTCCCACTGCAAAAGAGACGCAAGACGCAAGATAT	1688
QY	1873	AAGAAATGGAGACCACTGACTCATCTTCAGACTTTACCATGATATACCATGGCCA	1932
DB	1689	AAGAAATGGAGACCACTGACTCATCTTCAGACTTTACCATGATATACCATGGCCA	1748
QY	1933	CAGCCCTGAAGAGAGAAATCATCTATGTTAGAGAAATAGTAGCAATTTTGGAAATGCGAG	1992
DB	1749	CAGCCCTGAAGAGAGAAATCATCTATGTTAGAGAAATAGTAGCAATTTTGGAAATGCGAG	1808
QY	1993	TCCGAAGTCCGAGAGCGCTGGTCTATTTGGCAATTTCCAGAGCGGAATTCAGAGCGAAA	2052
DB	1809	TCCGAAGTCCGAGAGCGCTGGTCTATTTGGCAATTTCCAGAGCGGAATTCAGAGCGAAA	1868

QY 2053 AGAAGATCAGAGTGGATGATCATATCATCAGGACAGATCAAGGCTTCTGCTAGTAG 2112
Db |||||
QY 1869 AGAAGATCAGAGTGGATGATCATATCATCAGGACAGATCAAGGCTTCTGCTAGTAG 1928
Db |||||
QY 2113 TCTACACAGAGGATTCAGGCAATTAACCTCTGCCATCGGTGGAACATGGGTTTATACA 2172
Db |||||
QY 1929 TCTACACAGAGGATTCAGGCAATTAACCTCTGCCATCGGTGGAACATGGGTTTATACA 1988
Db |||||
QY 2173 AACTCTTTTAAAGTTAACCTCGAAGTCAATGACACAGAGCAATTTGGAAGAACTTCTTCA 2232
Db |||||
QY 1989 AACTCTTTTAAAGTTAACCTCGAAGTCAATGACACAGAGCAATTTGGAAGAACTTCTTCA 2048
Db |||||
QY 2233 TAAAGATGATGAGGATGGCTCTAAGACCAAGAAATGTCATAGCATGACACCTAG 2292
Db |||||
QY 2049 TAAAGATGATGAGGATGGCTCTAAGACCAAGAAATGTCATAGCATGACACCTAG 2108
Db |||||
QY 2293 CCAGAAGGCTCTGATCAGAGACTTCATGAGCTCATCAACCCCAATCTCAACACGAT 2352
Db |||||
QY 2353 GATGAGTCTCTGTAACAAAGTTTGGAAAGGACCGGAAACAACTCGGCAAGCCAGG 2412
Db |||||
QY 2169 GATGAGTCTCTGTAACAAAGTTTGGAAAGGACCGGAAACAACTCGGCAAGCCAGG 2228
Db |||||
QY 2413 ACATACCCAGGAAACAGTAAACAAATGGAAGCACTTACAGAAATGGAAGGTAGAAA 2472
Db |||||
QY 2229 ACATACCCAGGAAACAGTAAACAAATGGAAGCACTTACAGAAATGGAAGGTAGAAA 2288
Db |||||
QY 2473 CAGGAGGCCACGAAATTTAGAGGACCCAGGAGTGTCTGAGCTGCATTACCTCTAGA 2532
Db |||||
QY 2289 CAGGAGGCCACGAAATTTAGAGGACCCAGGAGTGTCTGAGCTGCATTACCTCTAGA 2348
Db |||||
QY 2533 AACCTCAACAGTAAAGTTCGCTAGACATACTGGAAGAAATGGAAGGTAGAAA 2592
Db |||||
QY 2349 AACCTCAACAGTAAAGTTCGCTAGACATACTGGAAGAAATGGAAGGTAGAAA 2408
Db |||||
QY 2593 GAACCTTTTCAAGCAATTAATGAGTGTGGAAGTTCGGAAGTTCGGAAGTTCGGAAGTTCGA 2652
Db |||||
QY 2409 GAACCTTTTCAAGCAATTAATGAGTGTGGAAGTTCGGAAGTTCGGAAGTTCGGAAGTTCGA 2468
Db |||||
QY 2653 CCAATTTAAATTAATCAATGAGTAACTTTCCTTAATAGGCTTTTTC 2702
Db |||||
QY 2469 CCAATTTAAATTAATCAATGAGTAACTTTCCTTAATAGGCTTTTTC 2518
Db |||||

RESULT 6

PCT-US94-10151A-53
; Sequence 53, Application PC/TUS9410151A
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: The Semaphorin Gene Family
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESS: FLHR HOBBACH TEST ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; City: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/10151A
; FILING DATE: 13-SEP-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: FP-58750-PC/RAO
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 272999 FRI UR
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2601 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 16..2331
PCT-US94-10151A-53

Query Match 92.6%; Score 2508.4; DB 5; Length 2601;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2509; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 193 CTGAGCATGGGCTGGTTAACTAGGATTGCTCTCTTTCTGGGGAGTATTACTTACAGC 252
Db 9 CTGAGCATGGGCTGGTTAACTAGGATTGCTCTCTTTCTGGGGAGTATTACTTACAGC 68
QY 253 AAGAGCAACTATCAGAAATGGGAAGAAACAATGTGCCAAGGCTGAAATTTATCTTACAAAGA 312
Db 69 AAGAGCAACTATCAGAAATGGGAAGAAACAATGTGCCAAGGCTGAAATTTATCTTACAAAGA 128
QY 313 AATGTTGGAATCCAAACAATGTGATCACTTTCAATGGCTTGGCCAAAGGCTTATCA 372
Db 129 AATGTTGGAATCCAAACAATGTGATCACTTTCAATGGCTTGGCCAAAGGCTTATCA 188
QY 373 TACCTTCTTTTGGATGAGGAACGGAGTAGGCTGTATGTTGGAGCAAGGATCACATATT 432
Db 189 TACCTTCTTTTGGATGAGGAACGGAGTAGGCTGTATGTTGGAGCAAGGATCACATATT 248
QY 433 TTCAATTCGACTGGTTAAATCAAGGATTTCAAGAGATTTGTTGGCCAGTATCTTACAC 492
Db 249 TTCAATTCGACTGGTTAAATCAAGGATTTCAAGAGATTTGTTGGCCAGTATCTTACAC 308
QY 493 CAGAAGAGATGAATGCAAGTGGGCTGGAAGAAACATCTGAAAGAAATGTCTAAATTTTCAT 552
Db 309 CAGAAGAGATGAATGCAAGTGGGCTGGAAGAAACATCTGAAAGAAATGTCTAAATTTTCAT 368
QY 553 CAAGGTACTTTAAGGCATATAATCAGACTCACTTTAGGCTGTGGAACGGGGCTTTTCA 612
Db 369 CAAGGTACTTTAAGGCATATAATCAGACTCACTTTAGGCTGTGGAACGGGGCTTTTCA 428
QY 613 TCCAAATTTGCACTCAATTTGAAATTCGACATCATCTGAGGACAAATATTTTAAAGCTGGA 672
Db 429 TCCAAATTTGCACTCAATTTGAAATTCGACATCATCTGAGGACAAATATTTTAAAGCTGGA 488
QY 673 GAACTCACATTTTGAAGAACGGCGGTGGGAAGAGTCCATATGACCCCTAAGCTGCTGACAGC 732
Db 489 GAACTCACATTTTGAAGAACGGCGGTGGGAAGAGTCCATATGACCCCTAAGCTGCTGACAGC 548
QY 733 ATCCCTTTTAAATAGATGGAGAAATTAACCTGGAAGTGGAGTGGAGTGGAGTGGAGTGGAG 792
Db 549 ATCCCTTTTAAATAGATGGAGAAATTAACCTGGAAGTGGAGTGGAGTGGAGTGGAGTGGAG 608
QY 793 CTTTGTCTATCTTCCGAACCTTTTGGGCAACCAACCAATCAGGACAGAGCAGCATGATTC 852
Db 609 CTTTGTCTATCTTCCGAACCTTTTGGGCAACCAACCAATCAGGACAGAGCAGCATGATTC 668
QY 853 CAGGTGGCTCAATGATCCAAAGTTCATTTAGTGGCCACCTCATCTCAGAGAGTGACATCC 912
Db 669 CAGGTGGCTCAATGATCCAAAGTTCATTTAGTGGCCACCTCATCTCAGAGAGTGACATCC 728
QY 913 TGAAGATGACAAAGTATATCTTTTCTCCGTGAAATGCAATAGATGGAAGACATCTTGG 972
Db 729 TGAAGATGACAAAGTATATCTTTTCTCCGTGAAATGCAATAGATGGAAGACATCTTGG 788
QY 973 AAAAGCTACTCAGCTAGATAGGTGAGATGCAAGATGATGCAAGATGATGCAAGATGCAAG 1032
Db |||||

TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1481 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: both
MOLECULE TYPE: cdna
FEATURE:
NAME/KEY: CDS
LOCATION: 50...1480
US-08-136-922-1

Query Match 52.2%; Score 1415.2; DB 1; Length 1481;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 1420; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 899 GAGAGTGCACATCTCGAAGATGACAAAGTATATCTTTTCTTCGTGAAATGCAATAGAT 958
Db 53 GAAATGACATCTCGAAGATGACAAAGTATATCTTTTCTTCGTGAAATGCAATAGAT 112
Qy 959 GGAGAACACTCTGAAAAGCTTACTCAGCTAGATAGTGTGATATGATATGCAAGATGACTTT 1018
Db 113 GGAGAACACTCTGAAAAGCTTACTCAGCTAGATAGTGTGATATGATATGCAAGATGACTTT 172
Qy 1019 GGAGGGACAGAGTCTGGTGAATTAATGACACATCTCTCAAGCTCTGCTGATTTGC 1078
Db 173 GGAGGGACAGAGTCTGGTGAATTAATGACACATCTCTCAAGCTCTGCTGATTTGC 232
Qy 1079 TCAGTGCAGGTCCAAATGGCATTTGACATCATTTTGTATGATGATGAGGATGATTTCTTA 1138
Db 233 TCAGTGCAGGTCCAAATGGCATTTGACATCATTTTGTATGATGATGAGGATGATTTCTTA 292
Qy 1139 ATGAATTTAAAGATCTTAAATTCAGTGTGATATGATGATGATGATGATGATGATGATGAT 1198
Db 293 ATGAATTTAAAGATCTTAAATTCAGTGTGATATGATGATGATGATGATGATGATGATGAT 352
Qy 1199 ATTTTCAAGGATCAGCGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1258
Db 353 ATTTTCAAGGATCAGCGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 412
Qy 1259 GGTCCATATGCCACAGGATGGACCAACTATCAATGGGTGCTTTATCAAGGAAGATC 1318
Db 413 GGTCCATATGCCACAGGATGGACCAACTATCAATGGGTGCTTTATCAAGGAAGATC 472
Qy 1319 CCCTATCCACGGCCAGGAACTTGCCAGCAAAACATTTGGTGTGATGATGATGATGATGATGAT 1378
Db 473 CCCTATCCACGGCCAGGAACTTGCCAGCAAAACATTTGGTGTGATGATGATGATGATGATGAT 532
Qy 1379 GACCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1438
Db 533 GACCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 592
Qy 1439 TTTCTATGAACAATCGCCCAATAGTATCAAAACGGATGTAATTTATCAATTTACACAA 1498
Db 593 TTTCTATGAACAATCGCCCAATAGTATCAAAACGGATGTAATTTATCAATTTACACAA 652
Qy 1499 ATTTGCTAGACCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1558
Db 653 ATTTGCTAGACCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 712
Qy 1559 GATGTTGGACCGTCTTTAAAGTATGTTTCAATTCCTAAGGAGATGATGATGATGATGATGATGAT 1618
Db 713 GATGTTGGACCGTCTTTAAAGTATGTTTCAATTCCTAAGGAGATGATGATGATGATGATGATGAT 772
Qy 1619 GAGGTTCTCTGGAGAAATGACATTTTTCGGAAACCGATGCTTATTTTCAGCATGAG 1678
Db 773 GAGGTTCTCTGGAGAAATGACATTTTTCGGAAACCGATGCTTATTTTCAGCATGAG 832
Qy 1679 CTTTCCACTAACGACCAACATATATTTGTTCAACGGTGGGGTTCGCCAGTCCCT 1738

Db 833 CTTTCCACTAACGACCAAACTATATATGTTCAACGGTGGGGTTGCCAGTCCCT 892
Qy 1739 TTACACCGTGTGATATTTACGGGAAAGCGTGTGCTGAGTGTGCTCGCCCGAGACCT 1798
Db 893 TTACACCGTGTGATATTTACGGGAAAGCGTGTGCTGAGTGTGCTCGCCCGAGACCT 952
Qy 1799 TACTGTGCTTGGGATGGTCTCTGCTATTTCTCGCTATTTTCCACTGCAAAAGAGACGACA 1859
Db 953 TACTGTGCTTGGGATGGTCTCTGCTATTTTCCACTGCAAAAGAGACGACA 1012
Qy 1859 AGACGACAGATATTAAGAAATGGAGACCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1918
Db 1013 AGACGACAGATATTAAGAAATGGAGACCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1072
Qy 1919 AATCACCATGGCCACAGCCCTCAAGAGAGAAATCATCTATGTTGTAGAGAAATAGTAGCACA 1978
Db 1073 AATCACCATGGCCACAGCCCTCAAGAGAGAAATCATCTATGTTGTAGAGAAATAGTAGCACA 1132
Qy 1979 TTTTGGATGACGTCGGAAGTCGAGAGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2038
Db 1133 TTTTGGATGACGTCGGAAGTCGAGAGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1192
Qy 2039 AATGAGAGCGGAAAGAGAGATCAGATGATGATGATGATGATGATGATGATGATGATGATGAT 2098
Db 1193 AATGAGAGCGGAAAGAGAGATCAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1252
Qy 2099 CTTTCTGCTAGTAGTCTACACAGAGAGATTCAGCAATTTACCTCTGCAATCGGTGGAA 2158
Db 1253 CTTTCTGCTAGTAGTCTACACAGAGAGATTCAGCAATTTACCTCTGCAATCGGTGGAA 1312
Qy 2159 CATGGTTTCATCAAACTCTTTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 2218
Db 1313 CATGGTTTCATCAAACTCTTTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 1372
Qy 2219 GAAGAACTTCTTCATAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2278
Db 1373 GAAGAACTTCTTCATAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1432
Qy 2279 AGCATGACACCTAGCCAGAGAGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2326
Db 1433 AGCATGACACCTAGCCAGAGAGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1480

RESULT 8
US-09-308-179B-2
; Sequence 2, Application US/09308179B
; Patent No. 6436669
; GENERAL INFORMATION:
; APPLICANT: INAGAKI, Shinobu
; APPLICANT: FURUYAMA, Tatsuo
; TITLE OF INVENTION: NOVEL SEMAPHORIN GENES (I)
; FILE REFERENCE: 0020-4562P
; CURRENT APPLICATION NUMBER: US/09/308,179B
; CURRENT FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: PCT/Jp97/04111
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: JAPAN 321068/1996
; PRIOR FILING DATE: 1996-11-15
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 2898
; TYPE: DNA
; ORGANISM: Mus sp.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(2898)
; OTHER INFORMATION: Strandedness: Double-stranded
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(2898)
; OTHER INFORMATION: any n = a, c, g, t, unknown, or other
US-09-308-179B-2

Query Match		22.08; Score 596.4; DB 4; Length 2898;
Best Local Similarity		56.3%; Pred. No. 4.5e-176;
Matches 1229; Conservative 0; Mismatches 911; Indels 24; Gaps 5;		
Qy	223	CTGTCTTTCTGGGGAGTATTACTTACAGCAAGAGCAAACTATCAGAAATGGGAAGAACAA 282
Db	396	CTTGCTCTCTGGGGTCACTGCTGGAACCTGGAACCCAGGTCATCTCGCGAACCCTC 455
Qy	283	TGTCGCAAGGTGAATATTCCTACAAAGAAATGTTGGAAATCCAAATGTGATCACTTT 342
Db	456	CTACCCGAGGTACGCTGTGCATATAAGAACTTTTGGAACTGAATAGGACTTCAATATT 515
Qy	343	CAATGGCTTGGCCAAACAGCTCCAGTTATCATCTTCTCTTGGATGAGGAACGGAGTAG 402
Db	516	TCAAAGCCCCCTTGGATTTCTTGNATCTCCATACATGCTGCTGGATGAGTATCAAGAACG 575
Qy	403	GCTGTATGTTGGCAAGAGATCACATATTTTCAATTCGACCTGCTGTTAATCA --- AGGA 459
Db	576	GCTCTTGTGGGCGCAGAGACCTTGTCTATTCCCTGAACTTGGAAACGAGTCAAGTACGG 635
Qy	460	TTTTCAAGATTTGTGGCCAGTATCTTACACAGAGAGATGAATGCAAGTGGGCTGG 519
Db	636	CTACAGAGATATCTGGGCGGAGCACAGCAGTAAGGTAGAAGATGCATATGAAGG 695
Qy	520	AAAAGACATCTGAAAGAAATGTGCTAATTTTCATCAAGGTACTTTAAGGCATATAATCAGAC 579
Db	696	AAAAGA --- CGCAATGAGTGTGCCAATATATATCCGGGTTTTCATCACTACAAACAGGAC 752
Qy	580	TCATTTGACGCTGTGGAGCGGGGCTTTTCAATCCAAATTTGCACCTACATTCGAATTTGG 639
Db	753	ACACCTTCTGACCTGTCTACTGAGCTTTTGTATCCACACTGTGCTCTCATCAGATCGG 812
Qy	640	ACATCATCTCTGAGGACAAATTTTAAAGCTGGAGAACTCACATTTTGAAGAACCGCCGTGG 699
Db	813	GCACCATTCAGAGAAACCCCTGTTTACCTGGAGTCACACAGATCTGAGAGAGAGGGG 872
Qy	700	GAAGAGTCCATATGACCTTAAGCTGTGACAGCATCCCTTTTAAATAGATGGAGAAATATA 759
Db	873	CAGATGTCTTTTACCCCACTCCTCTTTGTGCCACGCTAGTTGGGAATGAGCTGT 932
Qy	760	CTCTGGAACCTGCAGCTCATTTTATGGGCGAGACTTTGTCTATCTTCGGAACCTCTCGGCA 819
Db	933	TGCTGGACTCTACAGTGAATTTTGGGCGAGAGACTCGGCGAATTTTCGAGCATGGGAA 992
Qy	820	CCACCCCAATCAGGACAGCAGCATGATTCAGGTGCTCAATGATCCAAAGTTCAAT 879
Db	993	GTTAGGCCATATTCGCACCTGAGCATGACGATGAGCGCTCCTCAAGAAACCAAAATTTGT 1052
Qy	880	TAGTGGCCCACTCATCTCAGAGGTGACATCTCTGAGATGACAAAGTATATCTTTTCTT 939
Db	1053	AGGTTTCAATATGATTTCTCTATACGAAGACCGAGATGACAAATAATGTACTTTTCTT 1112
Qy	940	CCGTGAAATTCGAATAGATGGAGAACACTCTCGAAAGCTACTCACCGCTAGAAATAGGTCA 999
Db	1113	TACTGAGAGCGCTGGAGCGGAGAACACGCCACACGATCTACACCGAGTGGGGG 1172
Qy	1000	GATATGAAGAAATGACTTTTGGAGGCGACAGAACTCTGGTGAATTAATGACCAATCTCT 1059
Db	1173	GCTGTGGTGAATGACATGGAGGACAGAGAACTCTGGTGAACAAAGTGGAGCACTTTCTCT 1232
Qy	1060	CAAGCTCGTCTGATTTTGTCTCAGTCCAGGTCCAAATGGCATTTGACACTCAATTTGATGA 1119
Db	1233	TAAAGCGCGGCTGTTTGTCTCAGTGGCGGAAATGAATGATGACACATATCTTTCACGA 1292
Qy	1120	ACTGAGGATGATATTCCTAATGAATTTAAAGATCTTAAAGATCCCAAGTTGATATGAGT 1179
Db	1293	ACTAGAGGATGTGTTTAACTGTCGACAGAGATCTTAAAGATCCCAAGTATTTTGGACT 1352
Qy	1180	GTTTACGACTTCCAGTAAATTTTCAAGGATCAGCGCTGTGTATGTATAGCATGATGA 1239
Db	1353	GTTTAACTACTACAGCAATATTTTAGAGCGCATGCTGTATGTGTATCAATGTCAAG 1412

Qy	1240	TGTGAAAGGGTGTCTTGGTCCATATGCCACAGGGATGGACCCCACTATCAATGGGT 1299
Db	1413	TATCCGGGAAGCCTTTATGGCCCATATGCTCATAAAGAGGCCCTCAATACCACGTGC 1472
Qy	1300	GCCTTATCAAGAAAGAGTCCCTATCCAGGCCAGGAACCTTGTCCAGCAAAACATTTGG 1359
Db	1473	ACTATATGAAGGAAAGTCCCTATCCCAAGGCCCTGTTCTGTGTGCCAGCAAGTAAACGG 1532
Qy	1360	TGG --- TTTTCACTCTCAAAAGGACCTTCTGTATGATGTTATTAACCTTTGCAGAAATCA 1416
Db	1533	AGGCAGTATGAACCAACCAAGATTACCCCGATGACCCATCCGTTTCGAGGATGCA 1592
Qy	1417	TCCAGCCATGTACAATCCAGTGTTCCTATGAACAATGGCCCAATAGTATGATCAAAACGGA 1476
Db	1593	TCCTCTATGTATCAGCCCATAAACCTGTTCTATAAAAAACCAATCTGGTAAAAACAGA 1652
Qy	1477	TGTAATTTATCAATTTACAAATTTGCTAGACGGAGTGGATGCAGAAATGGACAGTA 1536
Db	1653	TGGAAATATCAACCTGAGGCAACTTGCCTGATCGGGTGGAGCGGAGATGGCCAGTA 1712
Qy	1537	TGATGTTATGTTTATCGGAAACAGATGTTGGACCGCTTCTTAAAGTAGTCTTCAATTCCTAA 1596
Db	1713	TGACGTCTTATTTATTTGGACAGACACAGGAATTTGTCTGAAAGTATCAATTTTACAA 1772
Qy	1597	GGAGACTTGTATGATTTAGAGAGGTTCTGCTGGAAGAAATGACAGTCTTTTCGGGAACC 1656
Db	1773	CCAAGAAACAGAGTGGATGGAGGAAGTCACTCTAGAGGAACTTCAAAATATTTCAAGGATCC 1832
Qy	1657	GACTGCTATTTTCAACAATGGAGCTTCCACTAAGCAGCAACAATATATATTTGTTTCAAC 1716
Db	1833	AGCCCTATCATTTCTATGGAATTTCTTCAAGAGACACAGCTTTTACATTGATCAGC 1892
Qy	1717	GGTGGGGTCCCGAGCTCCCTTTACACCGGTGTGATATTTACGGGAAAGCGTGTGCTGA 1776
Db	1893	CTCTGCTGTGGCACAAGTCAAGTCCATCTCACTGCGACATGTTATGGCAGTCTGTTGCTGA 1952
Qy	1777	GTGTTGCTCCCGGAGACCTTACTGCTGTGGGATGGTTCTGCTATGTTCTCGCTATTT 1836
Db	1953	CTGCTGCTGTGCTCGAGACCGTACTGCTGCTGGATGGCATATCTCTCTCCAGGTACTA 2012
Qy	1837	TCCACAC --- TGCAGAGACGCAACAAGACGCAAGATATAAGAAATGGAGACC 1887
Db	2013	CCCAACAGGTGCACACGCAAGAGAGAGGTTCCCGAGGACGACGTTCCGATGSCAACGC 2072
Qy	1888	ACTGACTCACTGTTTCAAGCTTACACATGATATCATCCATGGCCACAGCCCTGAGAGAG 1947
Db	2073	CGCCCAACAGTGTCTTTGGACAGCAATTTGTTGGAGACGCGTTGGACAGGACTGAAGAGAG 2132
Qy	1948	AATCATCTATGCTGTAGAGAAATAGTACACATTTTGGAAATGCAATGCGAAGTCCGAGAG 2007
Db	2133	GCTGGCTTATGCGATAGAGACACAGTACTCTGTTGGAATGACCCCGCATCACTACA 2192
Qy	2008	AGCGTGGTCTTATTTGGCAATTTCCAGAGCGGAATTAAGAGCGGAAAGAGAGATCAGAGT 2067
Db	2193	AGCAAAAGTCTATCTGGTTTGTACAGAAAGGACGCGACGTAAGAAAGAGAGGTTGAAGAC 2252
Qy	2068	GGATGATCATATCATCAGGACAGATCAAGGCTTCTGCTAGTAGTCTCAAAACAGAAAGGA 2127
Db	2253	GGATGACAGAGTGTGTAAGATGGAGTGGGCTTCTCTTCTCAGAGTACGCAAGTACAGA 2312
Qy	2128	TTGAGGCAATTAACCTCTGCCATCGCGTGGAAACATGGGTTTATCAAAACTCTTCTTAAGGT 2187
Db	2313	TGAGGAGACCTATTTTGGCCAGACAGTAGAACACAAATTTTGTCCATCTCTGCGCTAAAT 2372
Qy	2188	AACCTTGAAGTCAATTGACACAGAGCATTTTGGAGAACTTCTTTCATAAAGATGATGATG- 2246
Db	2373	CACCTTGGAGTGTGTCGAAGAGCATTAAGTGGAGGGCATGTTTTCATGAAGACCATGAAGA 2432
Qy	2247	-----GAGATGGCTCTTAAGACCAAGAAATGTCCAATAGCATGACACTTAGCCAGAGAGGT 2301
Db	2433	GGAAAGACATCAAGATGCTCCCTCCCTTAAAGCGGTATGTCTCAGGGGACAAAACC 2492
Qy	2302	CTGTCACAGAGACTTATGAGCTCATCAACCCCACTCAACCCCACTCAACAGCATGGATGAGTT 2361

Db 2493 GTGGTACAGGAATCTTGGAGCTGATGGCTACAGCAATCTCCAGAGAGTGAAGAATA 2552
 QY 2362 CTGTGAACAAAGTTTGGAAAAGGGA 2385
 Db 2553 CTGCGAAAAGTGTGGTGTACAGA 2576

RESULT 9
 US-09-976-594-1002
 ; Sequence 1002. Application US/09976594
 ; Patent No. 6673549
 ; GENERAL INFORMATION:
 ; APPLICANT: Furness, Michael
 ; APPLICANT: Buchbinder, Jenny
 ; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
 ; FILE REFERENCE: PA-0041 US
 ; CURRENT APPLICATION NUMBER: US/09/976,594
 ; CURRENT FILING DATE: 2001-10-12
 ; PRIOR APPLICATION NUMBER: 60/240,409
 ; PRIOR FILING DATE: 2000-10-12
 ; NUMBER OF SEQ ID NOS: 1143
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 1002
 ; LENGTH: 2278
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No. 6673549 411373.7
 US-09-976-594-1002

Query Match 4.6%; Score 125; DB 4; Length 2278;
 Best Local Similarity 50.5%; Pred. No. 2.2e-28;
 Matches 488; Conservative 0; Mismatches 440; Indels 39; Gaps 6;
 QY 689 AACGGCCCTGGGAAGAGTCCATATGACCCTAAGCTGTGACAGCATCCCTTTTAATAGAT 748
 Db 758 AGCGAATGCCAGATGCCATATGATGCCAAACATGCCAAGTTCACCTGTTGTCAGAT 817
 QY 749 GGAGAAATATCTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAG 808
 Db 818 GGAAAACTATATCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAG 877
 QY 809 ACTCTTGGGACCCACCCCAATCAGGACAGAGATGATCCAGTGGCTCAATGAT 868
 Db 878 AGTCTTGGAGAAAGCCCTACCTCGGACCGTCAAGCAGATTCAAATGGTGAAGAA 937
 QY 869 CAAAGTTTCAATGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAG 928
 Db 938 CCATATCTTGTTCAGGCGGTGA-----TTACGGAGATTATATC 976
 QY 929 TACTTTTCTTCCGTGAATGCAATAGATGAGAGCACTCTGGAAGAGTCACTCACGCT 988
 Db 977 TACTTCTTCTTCCAGGAATAGCAGTGGAGTATACACATGGGAAAGTATGTTTCCCA 1036
 QY 989 AGAATAGTTCAGATATGCAAGAAATGACTTTGGAGG---GCACAGAGTCTGGTGAATAA 1045
 Db 1037 AGAGTGGCTCAGTGTGTAAGAAATGATATGAGGAGATCTCAAGAGTCTCTGGAGAAACAG 1096
 QY 1046 TGGACAAATCTCTCAAGCTCTGATTTGCTCAGTGGCCAGTCCCAATGGGATTCAC 1105
 Db 1097 TGGACGCTCTTCTTCAAGGCGGCTTGAAGTCTCAGTCTCTG-----AGACTCTCAT 1150
 QY 1106 ACTCATTTTGTAGTAACTGAGAGATGATTTCTTAATGAATTTAAAGATCTTAAATAATCCA 1165
 Db 1151 TTTTATTTCATCTCCAGGAGTTACAGATGATGATTCGATATCAACGGGCGTAT--- 1207
 QY 1166 GTTGTATATGAGTGTATACGACTTCCAGATATATTTCAAGGATTCAGCGGTGATG 1225
 Db 1208 GTTGTCTTGGCAACGTTTCTACACCTTATACAGATCTCTGGGTCTGCACTCTGTGCC 1267
 QY 1226 TATAGCATGATGATGAGAGGGTGTTCCTTGTTCATATATGCCACAGGATGAGCCC 1285

Db 1268 TATGACATGCTTGACATTTGCCAGTGTTTTACTGGAGATTCAAGGAACAGAGTCTCCT 1327
 QY 1286 AACTATCAATGGGTGCC---TTATCAAGGAAGAGTCCCTATCCACGGCGAGGACTTGT 1342
 Db 1328 GATTCACCTGGACACACAGTTCCTGATGACAGAGTTCCTAAGCCACAGCCAGGTTGCTGT 1387
 QY 1343 CCCAGCAAA---ACATTTGGTGGTTTTCACCTCTACAAAGGACCTTCTCTGATGATTTATA 1399
 Db 1388 GCTGGCTCATCTCTCTTGAAGAAGATATGCAACCTCCATGATGATTCCTGATGATACCCCTG 1447
 QY 1400 ACCTTTGAAGAAGTCAATCCAGCCATGATCAATCCAGTGTTCCTATGAACATCGCCCA 1459
 Db 1448 AACTTTCATCAAGACGACCCGCTCATGATGAGGAGTCCCTCCATCTTCAACAGGCCA 1507
 QY 1460 ATAGTATGATCAAAAGGATGTAATTTATCAATTTACAAATTTGCTAGACCGAGTGGAT 1519
 Db 1508 TGGTTCCTGAGAAACAATGTCAGATCCGCTTACCAAAATTTGAGTGGACACACCTGCT 1567
 QY 1520 GCAGAAAGATGACAGTATGATGATTTATGTTATCGAAACAGATGTTGGACCGTCTTTAAA 1579
 Db 1568 GGGCCATATCAGATCAGACTGTGTTTCTGGGATCAGAGAGGGAATCATCTTGAAG 1627
 QY 1580 GTAGTTTCAATTCCTAAGAGACTTGGTATGATTTAGAGAGGTTCTCTGGAAGAAATG 1639
 Db 1628 TTTTGGCCAGAAATAGGAATAGTGTGTTTCTTAAATGACAGCCTTTTCTGGAGGAGATG 1687
 QY 1640 ACAGTTT 1646
 Db 1688 AGTGTTT 1694

RESULT 10
 US-09-077-940A-1
 ; Sequence 1. Application US/09077940A
 ; Patent No. 6576441
 ; GENERAL INFORMATION:
 ; APPLICANT: KIMURA, Toru et al.
 ; TITLE OF INVENTION: NOVEL SEMAPHORIN 2 AND GENE ENCODING THE SAME
 ; FILE REFERENCE: 0020-4426P
 ; CURRENT APPLICATION NUMBER: US/09/077,940A
 ; CURRENT FILING DATE: 1998-06-05
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: Patent in version 3.1
 ; SEQ ID NO 1
 ; LENGTH: 3692
 ; TYPE: DNA
 ; ORGANISM: Rattus norvegicus
 ; FEATURE:
 ; NAME/KEY: 5'UTR
 ; LOCATION: (1)..(18)
 ; OTHER INFORMATION:
 ; NAME/KEY: CDS
 ; LOCATION: (19)..(2682)
 ; OTHER INFORMATION:
 ; NAME/KEY: 3'UTR
 ; LOCATION: (2683)..(3653)
 ; OTHER INFORMATION:
 ; NAME/KEY: PolyA_site
 ; LOCATION: (3654)..(3692)
 ; OTHER INFORMATION:
 ; US-09-077-940A-1

Query Match 3.5%; Score 95.2; DB 4; Length 3692;
 Best Local Similarity 47.8%; Pred. No. 6.7e-19;
 Matches 431; Conservative 0; Mismatches 438; Indels 33; Gaps 4;
 QY 705 GTCCATATGACCTTAAGCTGCTGACAGCATCCCTTTTAATGATGAGAAATTAATCTCTG 764
 Db 542 GCCCTACGACCCCAAGCATGCCAATGTCGCCCTCTTCTCAGATGGATGCTCTTCCACAG 601
 QY 765 GAATGAGCTGATTTTATGCGGAGACATTTGCTATCTTCCGAATCTCTTGGGACACC 824

```

602 CCACAGTAAGTACTTCTAGCCATCGACGCTGTTATCTACCGTAGCTTGGGACCGGC 661
QY ACCCAATCAGACAGACAGATGATTCAGGTGGCTCAATGATCCAAAGTTCATAGTG 884
Db CACACTCGGCACAGTAAAGTACTCAAGTGGTTTAAAGAGCCATCTTTGTGCATG 721
QY CCCACCTCATCTCAGAGAGTGACAATCCTGAAGATGACAAAGATATCTTTCTTCGTCG 944
Db CGGTGGAGTGGGAG-----CCAGTCTACTTCTTCTTCGGG 760
QY AAAATGCAATAGATGGAGAACACTCTCGAAAAGCTACTCAGGTAGATAGGTGAGATAT 1004
Db AGATCGCCATGGAGTTAACTATCTGGAAGAGTGGTGTGCTCCGCTGGCCCGTGTAT 820
QY GCAGAAATGATTTGGAGGACACAGAG---TCTGGTGAATAAATGACACAACTTCTCA 1061
Db GCAAGAAATGATGGGCGGCTCCCGGCTGCTGGAGAGAGTGGACTTCTTCTCTGA 880
QY AAGCTCGTCTGATTTGCTCAGTGCAGGTCCAAATGGCAATGACACTCATTTTGAAGAC 1121
Db AGGCCCGGCTCACTGCTCGTGGCTGG-----GGACTCAGACTTCTACTTCAATGTAC 934
QY TGCAGGATGATTTCTTAATGACTTTAAAGATCTTAAGATCTTAATAATTCAGTTGTATGGAGTGT 1181
Db TGCAGGCTGTGACTGGTGTG---GTGAGCCCTTGGCGCGCTCCAGTGAATTTCTTGTCT 991
QY TTACGACTTCCAGTAACATTTTCAAGGATCAGCGGTGTCTATGTATAGCATGAGTGTG 1241
Db TCTCACTCTCAGACAGATCCCTGGCTCAGCTGTCTGTGCTTTGACATGACCAAG 1051
QY TGAGAGGGTGTCTTGGTTCATATGCCACAGGAGATGACCCAACTATCAATGGGTGC 1301
Db TGGTGTGTGTGTTTGAAGGCGCTTCCGGGAGCAGAGTCACTGAGTCAATCTGGACCC 1111
QY CTTATCAAGAGAGTCCCTATCTACCGGCGCAGGAATCTTCTCCAGCAAAACATTTGGTG 1361
Db CAGTGTCTGAGGACCAAGTACCAAGCCAGGCGCGGTCTGTGAGCGCCCGGTATGC 1171
QY GTTTTGACTCTACAAAGGACCTTCTGATGATGTTATTAACCTTTGCAAGAGTCAATCCAG 1421
Db AGTACACGATCCAAATGCGCTTCTGACGAGATTTCTCAACTTTGTAAGACCCACCCAC 1231
QY CCATGTACATCCAGTGTCTTCTATGAAATGCAATGCCCAATAGTATCAAAACGATGTAA 1481
Db TGATGGAGAGAGCGGTGCCCTCCCTGGGCCACTCGCCCTTGGATTTGTGAGAACTTCTGATAC 1291
QY ATTATCAATTTACAAATTTGTGTAGACCGAGTGGATGAGAGATGACAGATATGATG 1541
Db GGCACCACTGACCCGAGTGGCTGTGATGTGGGTGAGGCCCATGGGCAATCAGACAA 1351
QY TTATGTTTATCGGACAGATGTTGGGACCGTCTTAAAGTATGTTTCAATCTCCTAAGGAGA 1601
Db TAGTCTTCTTGGCTGTGAGGTTGGACAGTCTCAAAATCTCTTGTGAAGCCCAATGCCA 1411
QY 1602 CT 1603
Db 1412 GT 1413

```

RESULT 11

US-09-653-274-12
; Sequence 12, Application US/09653274
; Patent No. 6635742
; GENERAL INFORMATION:

; APPLICANT: Boyle, Bryan J
; APPLICANT: Yeung, George Y
; APPLICANT: Arterburn, Matthew C
; APPLICANT: Mize, Nancy K
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Drmanac, Radoje T
; TITLE OF INVENTION: Methods and Materials Relating to Semaphorin-Like
; TITLE OF INVENTION: Polypeptides and Polynucleotides

```

; FILE REFERENCE: HVS-23
; CURRENT APPLICATION NUMBER: US/09/653,274
; CURRENT FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-10
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO. 12
; LENGTH: 1923
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1923)
; US-09-653-274-12

```

```

Query Match      3.3%; Score 90.6; DB 4; Length 1923;
Best Local Similarity 49.0%; Pred. No. 1.2e-17;
Matches 444; Conservative 0; Mismatches 424; Indels 39; Gaps 6;

```

```

QY 692 GGCCTGGGAAGAGTCCATATGACCCCTAAGCTGCTGACAGCATCCCTTTTAATAGATGGA 751
Db 436 GGCCTGGCAAGATGCCCATTTGATGCCAGACAAACCAATGTTGCCCTCTTTGCTGTGGG 495
QY 752 GAATTATATCTCTGGAATGTCAGCTGATTTTATGGGCGAGACTTTTGCTATCTTCCGAAC 811
Db 496 AAGCTGTATTCTGCCACAGTGGCTGACTTCTTGGCCAGCGATGCCGTTAATTATCGAAGC 555
QY 812 CTGGGACACACCCCAATCAGACAGACAGATGATTCAGGTGGCTCAATGATGCCA 871
Db 556 ATGGGTGATGATCTGCTTCCGCTTCCGACAAATAATATGATTTCCAAATGGATAAAGAGCCA 615
QY 872 AAGTTTATTAGTGGCCCACTCATCTCAGAGAGTGACAAATCCTGAAGATGACAAAGATATAC 931
Db 616 CACTTCTTCATGC-----CATAGAATATGAAACTATGTCTAT 654
QY 932 TTTTCTTCCGTGAAATGCAATAGATGGAGAACACTCTGGAAGACTACTCAGCTAGA 991
Db 655 TTCTTCTTCCGAAATGCTGTGCTGCAACATAAATAATTTAGCAAGGTGTGTATTCCTCCG 714
QY 992 ATAGTTCAGATATGCAAGATGACTTTGGAGGG---CACAGAAGTCTGGTGAATAAATGG 1048
Db 715 GTGGCCCGCATATGTAAAGACGACATGGTGTGTTCCAGCGGGTCTTGGAGAACACTGG 774
QY 1049 ACAACATTTCTCAAGCTGCTGCTGATTTGCTCAGTGCAGGTCCAAATGGCAATGACACT 1108
Db 775 ACTTCATTTTAAAGGGTCCGCTGAACTGTTCTGCTCCCTGAGATCCGTTTTTCTAC--- 831
QY 1109 CATTTGATGAATGTCAGGATGATTTCTTAATGAACCTTTAAAGATCCTAAAAATCCAGTT 1168
Db 832 ---TTTGAATGTTCTGAGTCTATTACAGACATA---TACAAATCAATGCAATCCCACT 885
QY 1169 GTATATGAGTGTTTTACGACTTCCAGTAACATTTTCAAGGAGTACAGCCGTGTGTATGAT 1228
Db 886 GTGGTGGGGGTGTTTACACAGCAGTCAATAGACATCCCTGTTCTGCTGTGTGCAATTT 945
QY 1229 AGCATGATGATGTGAGAGGGTCTTCTTGGTCCATATGCCACAGGGATGGACCCCAAC 1288
Db 946 AGCATGATGATGTGAGAGGGTCTTCTTGGTCCATATGCCACAGGGATGGACCCCAAC 1005
QY 1289 TATCAATGGGTGCTTATC---AAGAGAGAGTCCCTTATCCAGCGCCAGGAATTTGTCCC 1345
Db 1006 TCTGTTGGACAGCAGTTCCTCCGAGACAAAGTGCCTAAAGCAAGGCTGTGCTGTGTGCA 1065
QY 1346 AGCAAAACATTT---GGTGGTTTGAATCTTCAAAAGGACCTTCTGTATGATGTTATACC 1402
Db 1066 AAACACGCGCTTGGCGAAGCTTATAAAACCTTCCATGATTTCCCGGATGAACTCTGTCA 1125
QY 1403 TTTGCAAGAAGTCAATCCAGCCATGTAATCCAGTGTCTTCTATGAACAATCGCCCAATA 1462
Db 1126 TTCAATCAATCTCATCCCTCATGAGTCTCTCCGCTTCCACCCATTCGCGATGAGCCCTGG 1185
QY 1463 GTGATCAAAACGAGTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1522

```

Db 1186 TTCAAAAGACTCGGTTCAGTACAGACTGACGGCCATCTCAGTGGACCATTCAGCCGGA 1245
Qy 1523 GAAGATGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1582
Db 1246 CCCTACAGAACTACACAGTATCTTTGTTGGCTCTGAGCTGGCATGTTAAAGTT 1305
Qy 1583 GTTTCAA 1589
Db 1306 CTGGCAA 1312

RESULT 12

US-09-653-274-5
; Sequence 5, Application US/09653274
; Patent No. 6635742
; GENERAL INFORMATION:
; APPLICANT: Boyle, Bryan J
; APPLICANT: Yeung, George Y
; APPLICANT: Arterburn, Matthew C
; APPLICANT: Mize, Nancy K
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Dmanac, Radoje T
; TITLE OF INVENTION: Methods and Materials Relating to Semaphorin-Like
; FILE REFERENCE: HVS-23
; CURRENT APPLICATION NUMBER: US/09/653,274
; CURRENT FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-10
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 3261
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-653-274-5

Query Match 3.3%; Score 90.6; DB 4; Length 3261;
Best Local Similarity 49.0%; Pred. No. 1.7e-17;
Matches 444; Conservative 0; Mismatches 424; Indels 39; Gaps 6;
Qy 692 GGCGTGGGAAGTCCATATGACCCCTAAGTGTGACAGATCCCTTTTAAATAGTGA 751
Db 484 GGCGTGGGAAGTCCATATGACCCCTAAGTGTGACAGATCCCTTTTAAATAGTGA 543
Qy 752 GAATTTATCTCTGGAACCTGACGCTGATTTTATGGGGGAGACTTTGCTATCTCCGAACT 811
Db 544 AAGCTGATTTCTGCCACAGTGGCTGACTTCTTGGCCAGGATCGGTTATTTATCGAAGC 603
Qy 812 CTGGGCAACCAACCCCAATCAGACAGAGATGATTCAGGTTGGCTCAATGATCCA 871
Db 604 ATGGTGTGATGATCTGCGCTTCGCACATAAATATGATTTCCAAATGGATAAAGAGCCA 663
Qy 872 AAGTTCAATAGTGGCCACCTCATCTCAGAGAGTGACATCTGAGAGATGACAAAGTATAC 931
Db 664 CACTTCTTCATGC-----CATGAATATGAACTATGCTAT 702
Qy 932 TTTTCTTTCCTGGAATGCAATAGATGGAACACTCTGGAAGAGTACTCAGCTAGA 991
Db 703 TTTCTTCTTCGGAATGCTGTGCAACATAATATTTAGCAAGGCTGTGATTTCCCGC 762
Qy 992 ATAGTTCAGATGCAAGATGACTTTGGAGG---CACAGAAGTCTGTTGAATAATGG 1048
Db 763 GTGGCCCGCATATGAAAGACAGATGGGTGTTCCCGAGCGGCTCTGGAGAACACTGG 822
Qy 1049 ACAACATTCCTCAAGCTGCTGTGATTTGCTCAGTGGCCAGGTCCAAATGGCAATGACACT 1108
Db 823 ACTTCATTTCTAAAGCTCGGCTGAACTGTCTGCTCCCTGGAGATCCGTTTTTCTAC--- 879
Qy 1109 CATTGTTGATGAACTCGAGATGATTTCTTATGAACTTTAAGATCTTAAATCCAGTT 1168

Db 880 ---TTTGATGTTTCTGAGTCTATTATACAGACATAA---TACAAATCAATGGCATCCCCACT 933
Qy 1169 GTATATGAGTGTGTTTACGACTTCCAGTAAACATTTTCAAGGGATCAGCCGTGTGTATGTAT 1228
Db 934 GTGGTGGGGTGTGTTTACCAAGAGTCAATAGCATCCCTGGTTCCTGTCTGTGTGCAATT 993
Qy 1229 AGCATGAGTGTGAGAAAGGTGTTCTTGTTCATATGCCCAAGAGATGGACCCCAAC 1288
Db 994 AGCATGGATGACATTTAAAGAGACGGTTTAAAGGAACAGAAAACCTCCAGAT 1053
Qy 1289 TATCAATGGTGCCTTATC---AAGGAAGAGTCCCTATCCAGCCAGGAACCTTGTCCC 1345
Db 1054 TCTGTTTGGACAGAGTTCCTCCGAAAGAGTCCCAAGCCAGAGCCCTGGCTGTGTGCA 1113
Qy 1346 AGCAAAACATTT---GGTGGTTTTGACTCTACAAAGGACCTTCTCGATGATGTTTAAACC 1402
Db 1114 AAACAGCGCTTGGCGAAGCTTTATAAACCTCCATCGATTTCCCGGATGAAACTCTGTCA 1173
Qy 1403 TTTGCAAGNAGTCAATCCAGCCATGACAAATCCAGTGTTCCTATGAACAATGCCCAATA 1462
Db 1174 TTTATCAAAATCTCATCCCTGATGAGTCTGCGTTCCACCCATGCGGATGAGCCCTGG 1233
Qy 1463 GTGATCAAAACGGATGTAATTTATCAATTTACAAATTTCTGTAGACCGAGTGGATGCA 1522
Db 1234 TTCAAAAGACTCGGTTCAGGTACAGACTGACGGCCATCTCAGTGGACCATTCAGCCGGA 1293
Qy 1523 GAAGATGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1582
Db 1294 CCCTACCAAGACTACACAGTCACTTTGTTGGCTCTGAAAGTGGCATGGTACTTAAAGTT 1353
Qy 1583 GTTTCAA 1589
Db 1354 CTGGCAA 1360

RESULT 13

US-09-653-274-3
; Sequence 3, Application US/09653274
; Patent No. 6635742
; GENERAL INFORMATION:
; APPLICANT: Boyle, Bryan J
; APPLICANT: Yeung, George Y
; APPLICANT: Arterburn, Matthew C
; APPLICANT: Mize, Nancy K
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Dmanac, Radoje T
; TITLE OF INVENTION: Methods and Materials Relating to Semaphorin-Like
; FILE REFERENCE: HVS-23
; CURRENT APPLICATION NUMBER: US/09/653,274
; CURRENT FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-10
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 3694
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: CDS
; LOCATION: (434) ..(3694)
US-09-653-274-3

Query Match 3.3%; Score 90.6; DB 4; Length 3694;
Best Local Similarity 49.0%; Pred. No. 1.8e-17;
Matches 444; Conservative 0; Mismatches 424; Indels 39; Gaps 6;
Qy 692 GGCGTGGGAAGTCCATATGACCCCTAAGTGTGCTGACAGCATCCCTTTTAAATAGTGA 751
Db 917 GGCGTGGCAAGTGGCCATTTGATGCGACAAACCAATGTTGCCCTCTTTGCTGATGGG 976

```

752 GAATTATACTCTGGAACCTGAGCTGATTTTATGGGCGAGACTTTGCTATCTTTCCGAAC 811
Dd      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
977 AAGCTGTATTCTGCCAGTGGCTGACTTCTTGGCAGCGATCCGGTTATTATCGAAGC 1036
Qy      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
812 CTTGGGACCAACCACCAATCAGGACAGACAGATGATTCAGGTGGCTCAATGATCA 871
Dd      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1037 ATGGGTGATGATCTGGCTTCGCACAAATAAATATGATTCCAAATGGATAAAGAGCCA 1096
Qy      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
872 AAGTTCAATAGTGGCCACCTCATCTCAGAGAGTGACAAATCCTGAAGATGACAAAGTATAC 931
Dd      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1097 CACTTTCTTCATGC-----CATGAATATGGAACATATGTTCTAT 1135
Qy      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
932 TTTTCTTCCTGGAAATGCAATAGATGGAGAACATCTCTGGAAGAGCTACTCAGCTAGA 991
Dd      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1136 TTCTTCTTTCGAGAAATCGCTGCGAACATAAATATTAGCAAGGCTGTGTATTCCTCCG 1195
Qy      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
992 ATAGTTCAGATATGCAAGATGACTTTTGGAGGG--CACAGAAGTCTGTGTGAATAATGG 1048
Dd      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1196 GTGCCCGCATATGTAACACGACATGGGTGTTCCAGCGGTCTTGAGAAACACTGG 1255
Qy      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1049 ACACATTCCTCAAGCTCTGTTGATTTGCTAGTCCAGGTCCAAATGGCAATGACAT 1108
Dd      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1256 ACTTCAATTCATAAGGCTGGCTGAACCTGTTCTGCTCCCTGGAGATCGGTTTTTCTAC--- 1312
Qy      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1109 CATTTGATGATGACGAGGATGATTCCTAATGAATTTAAAGATCCTTAAATCCAGTT 1168
Dd      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1313 ---TTTGATGTTCTGACGCTTATACAGACATAA---TACAAATCAATGGCATCCCACT 1366
Qy      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1169 GTATATGGAGTGTTCAGACTTCCAGTAACATTTCAAGGGATCAGCCGTGTATGTAT 1228
Dd      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1367 GTGTGCGGGTGTTCACGACGCTCAATAGCATCCCTGTTCTGCTGTGTCATTT 1426
Qy      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1229 AGCATAGTGTATGAGAGGGTGTTCCTTGTGTCATATGCCACAGGATGAGACCCAC 1288
Dd      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1427 AGCATGTGATGACATTTGAAAAGTATTTCAAGAGGACGGTTTAAAGAAACAGAAACTCCAGAT 1486
Qy      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1289 TATCAATGGGTGCTTATC---AAGGAAGAGTCCCTTATCCAGGCGCAGGAAGTCTGCCC 1345
Dd      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1487 TCTGTTTGGACAGAGTTCGGAAGACAAAGTGGCAAGCAAGGCTGGCTGTGTGCA 1546
Qy      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1346 AGCAAAACATTT---GGTGTGTTGACTCTCAAAAGACCTTCTCTGATGATGTATPACC 1402
Dd      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1547 AAACACGCGCTTCCGAAGCTTATAAAACCTCCATCGATTTCCGGATGAAACTCTGTCA 1606
Qy      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1403 TTTCCAGAGAGTATCCAGCCATGATCAATCCAGTGTTCCTATGAACATCCGCCAATA 1462
Dd      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1607 TTCAATCAATCTATCCCTGATGGACTCTGCCGTTCCACCCATGCCGATGAGCCCTGG 1666
Qy      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1463 GTGATCAAAACGGATGTAAATATCAATTTACACAAATTTGCTAGACCGAGTGGATGCA 1522
Dd      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1667 TTCACAAAGACTCGGGTCAGGTACAGACTACGGCCATCTCAGTGACCATTCAGCCGGA 1726
Qy      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1523 GAAGATGCAAGTATGATGTTATGTTTATCGGAACAGATGTTGGACCGTCTTAAAGTA 1582
Dd      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1727 CCTTACCAGAACTACACAGTCACTTTGTTGGCTCTGAAAGTGGCATGTTAAAGTT 1786
Qy      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1583 GTTTCAA 1589
Dd      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1787 CTGGCAA 1793

```

RESULT 14

US-09-300-958A-24
; Sequence 24, Application US/09300958A
; Patent No. 6495319
; GENERAL INFORMATION:
; APPLICANT: McClelland, Michael
; APPLICANT: Welsh, John
; APPLICANT: Trenkle, Thomas
; TITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets and Methods of
; FILE OF INVENTION: Using Same
; FILE REFERENCE: P-PH 3457
; CURRENT APPLICATION NUMBER: US/09/300,958A

```

; CURRENT FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/083,331
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: 60/098,070
; PRIOR FILING DATE: 1998-08-27
; PRIOR APPLICATION NUMBER: 60/118,624
; PRIOR FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 2433
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-300-958A-24

Query Match      3.1%; Score 84; DB 4; Length 2433;
Best Local Similarity 47.6%; Pred. No. 1.6e-15;
Matches 357; Conservative 0; Mismatches 375; Indels 18; Gaps 3;

Qy 356 AACAGCTCCAGTTATCATCTTCTCTTTGGATGAGGAACGGAGTAGCTGTATGTGGA 415
Dd 34 AACATCTCCAACTACACGGCCCTTCTCTGAGCCAGGATGGAAGACGCTGTATGTGGG 93
Qy 416 GCAAAGGATCACATATTTTCA-----TTGACCTGTGTTAATATCAAGGATTTT 463
Dd 94 GCCCGAGAGGCCCTTTTGGCACTTAACAGCAACCTCAGCTTCTGCCAGGGGGAGTAC 153
Qy 464 CAAAGATGTGTGGCCAGTATCTTACACAGAAAGAGATGAATGCAAGTGGGCTGGAATA 523
Dd 154 CAAGAGCTACTGTGGAGTGCAGATGCTCAACAGGAAGCAGCAGTGCAGCTTCAAGGGCAAG 213
Qy 524 GACATCCTGAAGATGTGCTAATTTTCATCAAGTACTTAAAGGCATATAATCAGACTCAC 583
Dd 214 GACCAAGCGTGTACTGTCAAACTACATCAAGATCTCTCTGCCACTCACAAGCAGCCAC 273
Qy 584 TTGACGCTCTGGAACGGGGCTTTTCATCCAAATTTGCACCTACATTTGAAATTTGGACAT 643
Dd 274 CTGCTCACCTGTGGCAGCGCGCTTCCAGCCCTGTGTGCTTACATTCACATAGCGAGC 333
Qy 644 CATCTGAGGACATATTTTAACTGAGGAGTCACTACATTTTGAACCGCCGCGGGAAG 703
Dd 334 TTTACTTTAGCCCA---AGATGAGCGCGGTAATGTCATCTCGAGGATGGCAAGGTCAT 390
Qy 704 AGTCCATATGACCTTAAGCTGCTCAGCAGCATCCCTTTTAAATAGATGAGAAATATATCTCT 763
Dd 391 TGTCCCTTTGACCCCACTTCAAGTCCACGCTCTGTGTGTTGATGCTGAGCTGTACACT 450
Qy 764 GGAATGCGAGCTGATTTTATGGGCGGAGACTTTGCTATCTTCCGAACTCTTGGCACCAC 823
Dd 451 GGAACAGTCACTAGTCTTCCAGGGAACGACCCAGCCATTTCCCGGAGCCAGAGTTCCCGC 510
Qy 824 CACCAATACGAGACAGACAGCAGCATGATTCAGGTGGTCAATG---ATCCAAAGTTTCAAT 880
Dd 511 CCCACCAAGACTGAGAGCTCCCTCAACTGGCTACAGACCCCTCCCTTTGTGGCTCGGCT 570
Qy 881 AGTCCCAACCTCATCTCAGAGAGTGAACAATCTCTGAAGATGACAAAGTATATCTTTTCTTC 940
Dd 571 ACGTCCCCCGAGAGCTGGGCGAGCCCATAGTGTATGATGATAGATCTACTTCTTCTTCTC 630
Qy 941 CGTGAATATGCAATAGATGGAGACACTCTGGAAGAACTACTCAGCTAGAAATAGGTCAG 1000
Dd 631 AGCGAGACGGCCAGAGAGTTGAGTTCTTTGAGAACACCATCTGCTGCCAGTTGCCGA 690
Qy 1001 ATATGCAAGAAATGATTTTGGAGGCGCACAGAGTCTGTGTGAATTAATGGAACAACTTCTC 1060
Dd 691 GTCTGTAAAGGCGGATGAGGTTGGAGAGCGGTGTTCAGCAAGACGCTGGACCTCTCTTCTC 750
Qy 1061 AAAGCTCGTCTGATTTGCTCAGTCCAGGT 1090
Dd 751 AAGGCTAGCTCTGTGCTCCCGCCCTGAT 780

```

US-08-556-422A-1

; Sequence 1, Application US/08556422A
; Patent No. 6576754
; GENERAL INFORMATION:
; APPLICANT: HALL, Kathryn T.
; APPLICANT: FREEMAN, Gordon J.
; APPLICANT: SCHULTZE, Joachim L.
; APPLICANT: BOUSSIOS, Vassiliki
; APPLICANT: NADLER, Lee M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING CD100 MOLECULES
; FILE REFERENCE: DFN-005C9A2
; CURRENT APPLICATION NUMBER: US/08/556.422A
; CURRENT FILING DATE: 1995-11-09
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4157
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (88)...(2673)
US-08-556-422A-1

Query Match 3.1%; Score 83.2; DB 4; Length 4157;

Best Local Similarity 49.0%; Pred. No. 4.2e-15;
Matches 619; Conservative 0; Mismatches 569; Indels 75; Gaps 12;

QY	352	GGCCAAAGCTCCAGTATATACCTCTCTTTGGATGAGGAACGGAGTAGCGTGTATGT	411
DB	219	GCCAGACATCTACACTACTCAGCTTCTGCTGAGCGAGGACGACACCTTGTACAT	278
QY	412	TGGAGCAAGATGCTAATTTTCATTCGACTCTGTTTAATAT---CAAGATTTTCAAAA	468
DB	279	AGGTCCCGGAGGGGCTTCGCTGTGAAGCACTCAACATCTCCGAGAGGAGCATGA	338
QY	459	GATTGTGGCCAGTATCTTACACAGAGAGATCAATGCAAGTGGGCTGGAAGACAT	528
DB	339	GGTGTATTGGAAGGCTCAGAGAGCAAAAAGCAAAATGTCCGAAAGGGGAAATCAA	398
QY	529	CCTGAAGAAGATGTCTAATTTTCATCAGGTACTTAAGGCATATATATCAGACTCTTGT	588
DB	399	ACAGACAGAGTGCCTCACTACATCCGGTGTCTGAGCGGCACTCAGCGCCACTTCCCTTTA	458
QY	589	CGCTGTGGAACGGGGCTTTTCATCCAAATTGCACTTACATTTGAATTTGACATCCTC	648
DB	459	CGTGTGGGACCAACGCAATTCACGCGGCTGTGACCACTGAATTAATC-----	512
QY	649	TGAGGACAAATATTTTAAAGCTGGAGAACTCACAATTTGAAAACGGCGCTGGGAAGATCC	708
DB	513	-----CTTTAAGTTTCTGGGAAAA-----TGAGATGGCAAGGAAGATGTC	557
QY	709	ATATGACCTAAGCTGTGACAGCATCCCTTTTAAATAGATGGAGAAATATCTCTGGAAC	768
DB	558	CTTTGACCCAGCACACAGCTACATCCGTCATGTTGATGGAGAACTTTATTCGGGGAC	617
QY	769	TGACGCTGATTTTATGGGGGAGACTTTGCTATCTTCGGAATCTTGGGCAACCAACCC	828
DB	618	GTGCTATATTTTGGGAAGTGAACCCATCATCTCCCGAAATCT---TCCACAGTCC	674
QY	829	AATCAGGACAGACAGCATGATTCAGGTGGCTCAATGATCCAAAGTTTCAATAGTGCCA	888
DB	675	TCAGGAGACAG---AATATGCAATCCCTTGGCTGAACGAGCTAGTTTCGTTTGTGTA	731
QY	889	CCTCAT-----CTCAGAGATGACAATCTCTGAAGATGACAAAGTATATCTTTCTT	939
DB	732	CGTATCCGAAAGCCAGACAGCCCGGCGGAGGATGACAGGGGTCTACTTCTTCTT	791
QY	940	CCGTGAAATGCAATAGATGGAACACTCTGGAAGAACTACTCAGCTAGAAATAGGTCA	999
DB	792	CACGAGGTGCTGTGGAGTATGATTTGTGTTGAGGTGCTGATCCACCGATAGCAAG	851
QY	1000	GATATGCAAGATGACTTTGGAGGCGCACAGAGTCTGGTGAATTAATGGAACAATCTCT	1059

Search completed: September 23, 2004, 01:36:28
Job time : 205 secs

This Page Blank (uspto)